

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3337	100.0	697	2	US-09-949-016-9660	Sequence 9660, Ap
2	3316	99.4	626	2	US-09-949-016-6776	Sequence 6776, Ap
3	1751	52.5	598	2	US-09-949-016-6699	Sequence 6699, Ap
4	1371	52.5	641	2	US-09-949-016-10338	Sequence 10338, A
5	1367	41.0	617	2	US-09-949-016-10263	Sequence 10263, A
6	659.5	19.8	300	2	US-09-277-078-2	Sequence 2, Appli
7	533.5	16.0	533	1	US-07-952-800-2	Sequence 2, Appli
8	530.5	15.9	448	2	US-09-949-016-8178	Sequence 8178, Ap
9	530.5	15.9	462	1	US-08-592-383-2	Sequence 2, Appli
10	530.5	15.9	462	1	US-08-095-7288-4	Sequence 4, Appli
11	530.5	15.9	462	4	PCY-US92-02320A-4	Sequence 4, Appli
12	530.5	15.9	525	2	US-08-764-870-7	Sequence 7, Appli
13	530.5	15.9	525	2	US-08-980-115-7	Sequence 7, Appli
14	530.5	15.9	533	2	US-08-216-592A-4	Sequence 4, Appli
15	530.5	15.9	577	2	US-09-949-016-11572	Sequence 11572, A
16	527.5	15.8	462	6	5171671-2	Patent No. 5171671
17	525.5	15.7	446	1	US-07-952-800-4	Sequence 4, Appli
18	524.5	15.7	448	2	US-08-216-592A-2	Sequence 2, Appli
19	516	15.5	403	1	US-08-592-383-4	Sequence 4, Appli
20	502	15.0	454	2	US-09-949-016-11665	Sequence 11665, A
21	502	15.0	462	1	US-08-336-408B-2	Sequence 2, Appli
22	502	15.0	462	2	US-08-764-870-6	Sequence 6, Appli
23	502	15.0	462	2	US-08-980-115-6	Sequence 6, Appli
24	502	15.0	462	2	US-10-329-668-10	Sequence 10, Appl
25	502	15.0	462	2	US-09-590-447-4	Sequence 4, Appli
26	502	15.0	462	4	PCY-US91-00399-2	Sequence 2, Appli
27	500.5	15.0	503	2	US-09-949-016-9851	Sequence 9851, Ap



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QY 267 ASSLLGESPLSPSPSSSSGEGTCAVCGDNAAACHYGVRTCEGCKGFFKRTVOKNAXY 326
|||
Db 240 ASQLL--DTQVPSPSRSGSPSNEGJCAVCGDNAAACHYGVRTCEGCKGFFKRTVOKNAXY 297
|||
QY 327 VCLANKNCVDKRRNRRCQYCRFQKCLSVGMVKEVVRTDSLKGRRLSPKPSPLQOQRP 386
|||
Db 298 VCLANKNCVDKRRNRRCQYCRFQKCLAVGMVKEVVRTDSLKGRRLSPKPSPLQOQRP 352
|||
QY 387 SOPSPPSPICMNNALVRLTDSPT--RDLDYSRY--CPTDQAAAGTDAHVQOQFYNLLTA 443
|||
Db 353 QEPSPPSPVSLISALVRAHVDNSNPAMTSLDYSRFQANPDYQMSGDDTQHIQOQFYDLLTG 412
|||
QY 444 SIDVRSWAEEKIPGFTDLPKEDQTLIESAFLELVRLSIRSNATAEDKVFVFCNGVLVLR 503
|||
Db 413 SWEIIRGWAEEKIPGADLPKADQDLFESAFLELVRLAYRSNPVEGKLIFCNGVVLVLR 472
|||
QY 504 LQCLRGFGWLDISKDFSLNLSQSLNLDIQAALCLALSALSMITERHGLKBPKEVEELCNKIT 563
|||
Db 473 LQCVRGFGWLDISIVFSSNLQNMNIDISAFSCIAALAMVTERHGLKBPKEVEELCNKIT 532
|||
QY 564 SSLKDHQ--SKGQALEPTE--SKVLGALVELRKICTLGLQRIEYFLYKLELDVSPSSIIDKLF 620
|||
Db 533 NCKLDHVTFNNGGLNRPNYLSKLGKLPRLTCTQGLQRIEYFLYKLELDVSPSSIIDKLF 592
|||
QY 621 LDTLPP 626
|||
Db 593 LDTLPP 598
|||
RESULT 4
US-09-949-016-10338
; Sequence 10338, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10338
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10338

Query Match 52.5%; Score 1751; DB 2; Length 617;
Best Local Similarity 54.5%; Pred. No. 1.1e-126;
Matches 363; Conservative 74; Mismatches 121; Indels 108; Gaps 18;

QY 1 MPCVQAQYSPSPGSSYAAQY----SSEYTEIMNPYTKLTMDLGSITEITATATSLP 56
|||
Db 20 MPCVQAQYSGSPGASPASQSYSHSGEYSSDFTLPEVFKFSMDLTWTEI--TATTSLP 77
|||
QY 57 SIFTFVEGYSNYELKPCSVYQM----QRPLKVEEGRAPSYHHHHHHHHHHHHHHHHH 112
|||
Db 78 SFTFMDNYSTGYDVKPCCLYQMFSLGQOQSIRKEDIQMHNYQOQSH----- 124
|||
QY 113 QQPSIPPASSPEDEVLP--STGMVFKQSPSPSTPTTPAPPPQAGALWDEALPSAPGCIAPGP 171
|||
Db 125 ----LPQS----EWMHSGSVYKPSPPPTPTTPTGQVQHSPPMWD-----PGS 167
|||
QY 172 LLDPPMKAVPT-----VAGARPLFLHFKPSPPHPPA-----PSPAG 207
|||
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Db 168 LHNPHQNVVATTHMIEQRKTPVSRSLSPFKSPGPPGTPVSSQCMRFDGFLHVPMPPEPAG 227
|||
QY 208 GHILGYDPTAAALSLPLCAAAAAGSQAALSHHPYGLP--LAKRAAPLAPPLGLTTPSPT 266
|||
Db 228 SHV-----VDGQTFEAVNPPIRKPSMGFPGLQI---GH 258
|||
QY 267 ASSLLGESPLSPSPSSSSGEGTCAVCGDNAAACHYGVRTCEGCKGFFKRTVOKNAXY 326
|||
Db 259 ASQLL--DTQVPSPSRSGSPSNEGJCAVCGDNAAACHYGVRTCEGCKGFFKRTVOKNAXY 316
|||
QY 327 VCLANKNCVDKRRNRRCQYCRFQKCLSVGMVKEVVRTDSLKGRRLSPKPSPLQOQRP 386
|||
Db 317 VCLANKNCVDKRRNRRCQYCRFQKCLAVGMVKEVVRTDSLKGRRLSPKPSPLQOQRP 371
|||
QY 387 SOPSPPSPICMNNALVRLTDSPT--RDLDYSRY--CPTDQAAAGTDAHVQOQFYNLLTA 443
|||
Db 372 QEPSPPSPVSLISALVRAHVDNSNPAMTSLDYSRFQANPDYQMSGDDTQHIQOQFYDLLTG 431
|||
QY 444 SIDVRSWAEEKIPGFTDLPKEDQTLIESAFLELVRLSIRSNATAEDKVFVFCNGVLVLR 503
|||
Db 432 SWEIIRGWAEEKIPGADLPKADQDLFESAFLELVRLAYRSNPVEGKLIFCNGVVLVLR 491
|||
QY 504 LQCLRGFGWLDISKDFSLNLSQSLNLDIQAALCLALSALSMITERHGLKBPKEVEELCNKIT 563
|||
Db 492 LQCVRGFGWLDISIVFSSNLQNMNIDISAFSCIAALAMVTERHGLKBPKEVEELCNKIT 551
|||
QY 564 SSLKDHQ--SKGQALEPTE--SKVLGALVELRKICTLGLQRIEYFLYKLELDVSPSSIIDKLF 620
|||
Db 552 NCKLDHVTFNNGGLNRPNYLSKLGKLPRLTCTQGLQRIEYFLYKLELDVSPSSIIDKLF 611
|||
QY 621 LDTLPP 626
|||
Db 612 LDTLPP 617
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RESULT 5
US-09-949-016-10263
; Sequence 10263, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10263
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10263

Query Match 41.0%; Score 1367; DB 2; Length 641;
Best Local Similarity 47.5%; Pred. No. 4.8e-97;
Matches 317; Conservative 74; Mismatches 165; Indels 112; Gaps 23;

QY 1 MPCVQAQY----SPSPGSSYAAQYYSSEYTEIMNPYTKLTMDLGSITEITATATSLP 57
|||
Db 44 MPCVQAQYGTGAPSPGPDHLA-----SDPLTPEFIKPTMDLASPEAAPAAPTALPS 95
|||
QY 58 SIFTFVEGYSNYELKPCSVYQM----RPLKVEEGRAPSYHHHHHHHHHHHHHHHHH 114
|||
Db 96 FSTFMDGYTGEFD---TFLYQLPGTVQPCSSASSASSSTSSSSATSPASAFKPEDQVY 152
|||
QY 115 PSIP-PASSPEDEVLPSTSMVFKQSPPS--TPTTPAF-PPQAG----- 153
|||
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153 GYCPGLSPVDEALSSGSDYSGPCAPSPSTFSFPQLSPMDGSGFHSPSQTYEG 212  
154 -ALWDEALPSAGCIAPGLDPPMKAVTVPAGAPPLFHFHFKSPSPHPAPSPAGGHLG 212  
213 LRAMTEQLPKASG-----PPQ-----PPAFTSFSPTGSPS----- 244  
213 YDPTAAALSL-PLGAAAAAGSQAALSHHPYGLPLAKRAAPLAFFPLGLTPSPASSLL 271  
245 ---LAQSPKLKPPSQAATHQLG-----EGESYSM-----PTAPPGL-----APTSPLH 284  
272 G-----ESPSPSPSPSSSSG---EGTCVACGDNAAACQHYGVRTCEGCKGFFKRTVQKNK 325  
285 GSGILDTP-VYSTKARSGAPGSEGRCAVCGDNASCQHYGVRTCEGCKGFFKRTVQKNK 343  
326 YVCLANKCPVDKRRNRQCYCRQKCLSVGMVKEVVRTDSLKGRRLPLSPKPSPLQOE 385  
344 YICLANKCPVDKRRNRQCFRCFKCLAVGMVKEVVRTDSLKGRRLPLSPKPKQP----- 399  
386 PSQSPSPSPSPICMNAALVRLTDTSTP--RDLDYSRYCPTDQAAAG-TDAEHVQOQFYNLIT 442  
400 -----PDASPAALLTSLVRAHLDSGFSTAKLDYSKFQELVLPHFGKEDAGDVQOQFYDLS 454  
443 ASIDVSRGWAELIPGFTDLPKEDOTLLIESAFLELFLVRLRSIRSNATBDKPFVFCNGLVLH 502  
455 GSLEWIRKWAELIPGFAELSPADQDILLIESAFLELFLVRLRSIRSGEGLIFCSGLVLH 514  
503 RIQCLRGGEWLDISKPSLNLQSLNLDIQAALCLASLMSITERHGLKPKRVEBLCKNI 562  
515 RIQCARGFGDWDTSILAFSRLSHSLVDVPAFCLLSLVLTDRHGLQEPVRVEELQRI 574  
563 TSSLKHQSKGALPTE-----SKVLGALVELRKICTLGLQRIFFVYKLELDLYSPPSIIDK 618  
575 ASCLKEHVA-AVAGEFPQAPASCLRLGLKLPRLTLCQGLQRIFFVYKLELDLYSPPSIIDK 633  
619 LFLDTLPP 626  
634 IFMDTLPP 641

RESULT 6  
US-09-277-078-2  
; Sequence 2, Application US/09277078  
; Patent No. 6312949  
; GENERAL INFORMATION:  
; APPLICANT: Sakurada, Kazuhiro  
; APPLICANT: Palmer, Theo  
; TITLE OF INVENTION: REGULATION OF TYROSINE HYDROXYLASE  
; FILE OF INVENTION: EXPRESSION  
; FILE REFERENCE: 07251/031001  
; CURRENT APPLICATION NUMBER: US/09/277,078  
; CURRENT FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-277-078-2

Query Match 19.8%; Score 659.5; DB 2; Length 300;  
Best Local Similarity 41.6%; Pred. No. 6.6e-43;  
Matches 151; Conservative 41; Mismatches 74; Indels 97; Gaps 13;

QY 1 MFCVQAQYSPSPGGSYAAQTY-----SSRYTTEIMNPYTKLTMOLGSTEITATATTSIP 56  
DB 1 MFCVQAQYSSPQGSASQSYSHSSGYSDFLTPFVKESMDLTWTEI--TATTSIP 58  
QY 57 S1STFVGVSSNYELKPSCVYQM----QRPLIKVEGRAPSYHHHHHHHHHHHHHHHHH 112  
DB 59 SPSTFMDNSTGYDKPFPKCLYQMPLSGQGSQSIKVEDIQMHNTQOHS----- 105

113 QQSIPIBPASSPEDEVLIP-STSMYFKQSPSPSTPTTAPPPQAGALWDEALPSAPGCIAPGP 171  
106 ---LPQSP-----EEMPHSGSVYIKSPSPPTTPTPGFQVQHSPPMDD-----PES 148  
172 LLDPPMKAVPT-----VAGARFPFLFHFHFKSPSPHPPA-----PSPAG 207  
149 LNFHQNIVATTHMIEQKRTVPSRLSLFSFKQSPPGTVPVSSCQMRFDGDLHVPNNPEPAG 208  
208 GHHLGYDPTAAALSLPLGAAAAAGSQAALSHHPYGLP-LAKRAAPLAFFPLGLTPSPPT 266  
209 SHV-----LDGQTEAVPNPIRKPASMGFFGLQI---GH 239  
267 ASSLLGESPSLSPSSSSSGEGTCVACGDNAAACQHYGVRTCEGCKGFFKRTVQKNK 326  
240 ASQLL--DTQVPSPPSRGSPSNEGLCAVCGDNAAACQHYGVRTCEGCKGFFKRTVQKNK 297  
327 VCL 329  
298 VCL 300

RESULT 7  
US-07-952-800-2  
; Sequence 2, Application US/07952800  
; Patent No. 5403925  
; GENERAL INFORMATION:  
; APPLICANT: OZATO, KEIKO  
; TITLE OF INVENTION: A NEW MEMBER OF THE NUCLEAR HORMONE  
; TITLE OF INVENTION: RECEPTOR SUPERFAMILY AND A CDNA CLONE THEREOF  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND AND TOWNSEND  
; STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000  
; CITY: SAN FRANCISCO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/952,800  
; FILING DATE: 19920928  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 15280-21-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-543-9600  
; TELEFAX: 415-543-5043  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 533 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-952-800-2

Query Match 16.0%; Score 533.5; DB 1; Length 533;  
Best Local Similarity 29.7%; Pred. No. 7.3e-33;  
Matches 151; Conservative 70; Mismatches 189; Indels 99; Gaps 17;

QY 118 PPASSPEDEVLIPSTSMYFKQSPSPSTPTTAPPPQAGALWDEALPSAPGCIAPGLDPPM 177  
DB 83 PDSGSPNP--LP-----QGVPPSPSPGPPPLPSTA-----PSLGGSGAGPPP---PPM 124  
QY 178 KAVPTVAGARPLFHFHFKSPSPHPAPSPAGGHLGYDPTAAALSLPLGAAAAAGSQA 237  
DB 125 P--PPPLGSPFPVVISSSMGSPGLPPPPAPPGFSGPVSSPQINSVSLPGGSG----- 174

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	3337	100.0	626	4	US-10-608-863-2	Sequence 2, Appli	
2	3333	99.9	626	3	US-09-853-386-64	Sequence 64, Appl	
3	3333	99.9	626	4	US-10-414-080-14	Sequence 14, Appl	
4	3316	99.4	626	3	US-09-853-386-65	Sequence 65, Appl	
5	3316	99.4	626	3	US-09-853-386-96	Sequence 96, Appl	
6	3316	99.4	626	5	US-10-659-004-116	Sequence 116, Appl	
7	3299.5	98.9	625	3	US-09-853-386-63	Sequence 63, Appl	
8	3299.5	98.9	625	4	US-10-414-080-13	Sequence 13, Appl	
9	3133.5	93.9	643	3	US-09-853-386-70	Sequence 70, Appl	
10	3133.5	93.9	643	4	US-10-414-080-17	Sequence 17, Appl	
11	3123	93.6	587	4	US-10-755-889-64	Sequence 64, Appl	
12	3074	92.1	628	3	US-09-853-386-66	Sequence 66, Appl	
13	3074	92.1	628	3	US-09-853-386-68	Sequence 68, Appl	
14	3074	92.1	628	3	US-09-853-386-73	Sequence 73, Appl	
15	3074	92.1	628	4	US-10-005-169-4	Sequence 4, Appli	
16	3074	92.1	628	4	US-10-414-080-15	Sequence 15, Appl	
17	3054.5	91.5	627	3	US-09-853-386-67	Sequence 67, Appl	
18	3054.5	91.5	627	4	US-10-005-169-2	Sequence 2, Appli	
19	2099.5	62.9	446	3	US-09-853-386-69	Sequence 69, Appl	
20	2099.5	62.9	446	4	US-10-414-080-16	Sequence 16, Appl	
21	1751	52.5	598	3	US-09-853-386-37	Sequence 37, Appl	
22	1751	52.5	598	3	US-09-853-386-38	Sequence 38, Appl	
23	1751	52.5	598	3	US-09-853-386-39	Sequence 39, Appl	
24	1751	52.5	598	3	US-09-853-386-41	Sequence 41, Appl	
25	1751	52.5	598	4	US-10-205-951-2	Sequence 2, Appli	
26	1751	52.5	598	4	US-10-205-951-75	Sequence 75, Appl	
27	1751	52.5	598	4	US-10-205-951-79	Sequence 79, Appl	









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QY 121 SSPDEVLPSTSMYFKQSPSPSTPTTAPPPQAGALWDEALPSAPGCIAPGPIIDPPMKAV 180
D 121 SSPDEVLPSTSMYFKQSPSPSTPTTAPPPQAGALWDEALPSAPGCIAPGPIIDPPMKAV 180
QY 181 PTVAGARPLFHFKPSPPHPPAPSPAGGHHILGYDPTAAALSLPLGAAAAAGSQAALLES 240
D 181 PTVAGARPLFHFKPSPPHPPAPSPAGGHHILGYDPTAAALSLPLGAAAAAGSQAALLES 240
QY 241 HPYGLPLAKRAAPLAPPLGLTPSTASSLLGESPSLPPSRSSSGEGTCAVCGDNAA 300
D 241 HPYGLPLAKRAAPLAPPLGLTPSTASSLLGESPSLPPSRSSSGEGTCAVCGDNAA 300
QY 301 COHGVRTCEGCKGFFKRTVQKNKYVCLANKNCVDRKRRNRCCYCRFKCLSVGMVKE 360
D 301 COHGVRTCEGCKGFFKRTVQKNKYVCLANKNCVDRKRRNRCCYCRFKCLSVGMVKE 360
QY 361 VVRTDSLKGRGRRLPSKPSLQOEPPSPQSPSPPICMNNALVRALTDTSTPRDLDSRYC 420
D 361 VVRTDSLKGRGRRLPSKPSLQOEPPSPQSPSPPICMNNALVRALTDTSTPRDLDSRYC 420
QY 421 PTQAAAGTDAHVQOQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLTLLIESAFLEL-VL 480
D 421 PTQAAAGTDAHVQOQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLTLLIESAFLEL-VL 479
QY 481 RLSIRSNATDAEKFVFCNGLVLRLOCLRGFGEWLDISKDFSLNLSLNDLQALACTSAL 540
D 481 RLSIRSNATDAEKFVFCNGLVLRLOCLRGFGEWLDISKDFSLNLSLNDLQALACTSAL 539
QY 541 SMITERHGLKPKRVEELCNKITSSLDKHQSGQALEPTESKVLGALVELRKICTLGLQR 600
D 541 SMITERHGLKPKRVEELCNKITSSLDKHQSGQALEPTESKVLGALVELRKICTLGLQR 599
QY 601 IFYKLDELVSPPSIIDKFLDITLPP 626
D 601 IFYKLDELVSPPSIIDKFLDITLPP 625
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RESULT 8
US-10-414-080-13
; Sequence 13, Application US/10414080
; Publication No. US20030220288A1
; GENERAL INFORMATION:
; APPLICANT: MULLICAN, SHANNON E.
; APPLICANT: CONNELLY, ORLA M.
; APPLICANT: MILBRANDT, JEFFREY
; TITLE OF INVENTION: NOR-1 AND NUR77 NUCLEAR RECEPTORS AS TARGETS FOR
; TITLE OF INVENTION: ANTI-LEUKEMIA THERAPY
; FILE REFERENCE: P02454US1
; CURRENT APPLICATION NUMBER: US/10/414,080
; PRIOR FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/373,238
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-414-080-13
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Query Match 98.9%; Score 3299.5; DB 4; Length 625;
Best Local Similarity 99.2%; Pred. No. 8.6e-215;
Matches 621; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 MPCVQAOYSPSPGSSVAAQYTSSEYTTIMNPDYTKLTMDLGSSTEITATATSLPSIST 60
D 1 MPCVQAOYSPSPGSSVAAQYTSSEYTTIMNPDYTKLTMDLGSSTEITATATSLPSIST 60
QY 61 FVEGYSNYELKPCSCVYQMORPLIKVEGRAPSYHHHHHHHHHHHHHHHHHHHHHHHHHH 120
D 61 FVEGYSNYELKPCSCVYQMORPLIKVEGRAPSYHHHHHHHHHHHHHHHHHHHHHHHHHH 120
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QY 121 SSPDEVLPSTSMYFKQSPSPSTPTTAPPPQAGALWDEALPSAPGCIAPGPIIDPPMKAV 180
D 121 SSPDEVLPSTSMYFKQSPSPSTPTTAPPPQAGALWDEALPSAPGCIAPGPIIDPPMKAV 180
QY 181 PTVAGARPLFHFKPSPPHPPAPSPAGGHHILGYDPTAAALSLPLGAAAAAGSQAALLES 240
D 181 PTVAGARPLFHFKPSPPHPPAPSPAGGHHILGYDPTAAALSLPLGAAAAAGSQAALLES 240
QY 241 HPYGLPLAKRAAPLAPPLGLTPSTASSLLGESPSLPPSRSSSGEGTCAVCGDNAA 300
D 241 HPYGLPLAKRAAPLAPPLGLTPSTASSLLGESPSLPPSRSSSGEGTCAVCGDNAA 300
QY 301 COHGVRTCEGCKGFFKRTVQKNKYVCLANKNCVDRKRRNRCCYCRFKCLSVGMVKE 360
D 301 COHGVRTCEGCKGFFKRTVQKNKYVCLANKNCVDRKRRNRCCYCRFKCLSVGMVKE 360
QY 361 VVRTDSLKGRGRRLPSKPSLQOEPPSPQSPSPPICMNNALVRALTDTSTPRDLDSRYC 420
D 361 VVRTDSLKGRGRRLPSKPSLQOEPPSPQSPSPPICMNNALVRALTDTSTPRDLDSRYC 420
QY 421 PTQAAAGTDAHVQOQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLTLLIESAFLEL-VL 480
D 421 PTQAAAGTDAHVQOQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLTLLIESAFLEL-VL 479
QY 481 RLSIRSNATDAEKFVFCNGLVLRLOCLRGFGEWLDISKDFSLNLSLNDLQALACTSAL 540
D 481 RLSIRSNATDAEKFVFCNGLVLRLOCLRGFGEWLDISKDFSLNLSLNDLQALACTSAL 539
QY 541 SMITERHGLKPKRVEELCNKITSSLDKHQSGQALEPTESKVLGALVELRKICTLGLQR 600
D 541 SMITERHGLKPKRVEELCNKITSSLDKHQSGQALEPTESKVLGALVELRKICTLGLQR 599
QY 601 IFYKLDELVSPPSIIDKFLDITLPP 626
D 601 IFYKLDELVSPPSIIDKFLDITLPP 625
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RESULT 9
US-09-853-386-70
; Sequence 70, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnihan, Barry
; APPLICANT: Connelly, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
; TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
; FILE REFERENCE: P01972US1
; CURRENT APPLICATION NUMBER: US/09/853,386
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/203645
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-853-386-70
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Query Match 93.9%; Score 3133.5; DB 3; Length 643;
Best Local Similarity 92.4%; Pred. No. 1.5e-203;
Matches 594; Conservative 10; Mismatches 22; Indels 17; Gaps 3;
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QY 1 MPCVQAOYSPSPGSSVAAQYTSSEYTTIMNPDYTKLTMDLGSSTEITATATSLPSIST 60
D 1 MPCVQAOYSPSPGSSVAAQYTSSEYTTIMNPDYTKLTMDLGSSTEITATATSLPSIST 60
QY 61 FVEGYSNYELKPCSCVYQMORPLIKVEGRAPSYHHHHHHHHHHHHHHHHHHHHHHHHHH 110
D 61 FVEGYSNYELKPCSCVYQMORPLIKVEGRAPSYHHHHHHHHHHHHHHHHHHHHHHHHHH 120
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QY 111 --OHCQPSIPASSPEDEVLPSTSMYFKQSPSTTTTTPAFPQAGALWDEALPSAPGCGIA 168  
Db 121 PPQQQPSIPPPSGPEDEVLPSTSMYFKQSPSTTTTTPFPQAGALWDEALPSAQGCGIA 180  
QY 169 PGPILLDPPMKAVPTVAGARFPLFHFHFKPSPHPHPPAPSPAGGHHGLGYDPTAAAALSLPLG-- 226  
Db 181 PGPILLDPPMKAVPTVAGARFPLFHFHFKPSPHPHPPAPSPAGGHHGLGYDPTAAAALGLPLGAA 240  
QY 227 ---AAAAAGSQAALSHPHYGLPLAKRAAPLAPPLGLTPTSPASSLLGESPSLPSPSR 283  
Db 241 AAAAAAGSQAALSHPHYGLPLAKRAAALAFSPGLTPTSPASSLLGESPSLPSPSR 300  
QY 284 SSSSGEGTCVCGNNAACQHYGVRTCEGCKGFFKRTVQKNKYVCLANKNCVVKRRNR 343  
Db 301 STASGEGTCVCGNNAACQHYGVRTCEGCKGFFKRTVQKNKYVCLANKNCVVKRRNR 360  
QY 344 QYCRFQKCLSVGMVKEVVRTDSLGRRGRPLSPKPSPLQEPSPSPSPPICMNNALV 403  
Db 361 QYCRFQKCLSVGMVKEVVRTDSLGRRGRPLSPKPSPLQEPSPSPSPPICMNNALV 420  
QY 404 RALTDSTPRDLSDYRYCPTDQAAAGTDAEHVQOQFVNLTTASIDVSRSWAEKIPGFTDLPK 463  
Db 421 RALTDSTPRDLSDYRYCPTDQAAAGTDAEHVQOQFVNLTTASIDVSRSWAEKIPGFTDLPK 480  
QY 464 EDQTLLESFALEFLVLRSLRSNTAEDKFVFCNGLVLRQLRQCLRGFGEWLDISKDFSLN 523  
Db 481 EDQTLLESFALEFLVLRSLRSNTAEDKFVFCNGLVLRQLRQCLRGFGEWLDISKDFSLR 540  
QY 524 LQSLNLDIQALACLALSALSMITERHGLKEPKRVEELCNKITSSLDKHQSKGQALEPTESKV 583  
Db 541 LQSLNLDIQALACLALSALSMITERHGLKEPKRVEELCNKITSSLDKHQSKGQALEPTEPKV 600  
QY 584 LGALVELRKICTLGLQRIFYKLEDLVSPPSIIDKFLDITLPP 626  
Db 601 LRALVELRKICTLGLQRIFYKLEDLVSPPSIIDKFLDITLPP 643

RESULT 10  
US-10-414-080-17  
; Sequence 17, Application US/10414080  
; Publication No. US20030220288A1  
; GENERAL INFORMATION:  
; APPLICANT: MULLICAN, SHANNON M.  
; APPLICANT: CONNEELY, ORLA M.  
; APPLICANT: MILBRANDT, JEFFREY  
; TITLE OF INVENTION: NOR-1 AND NUR77 NUCLEAR RECEPTORS AS TARGETS FOR  
; FILE REFERENCE: P02454US1  
; CURRENT APPLICATION NUMBER: US/10/414,080  
; CURRENT FILING DATE: 2003-04-15  
; PRIOR FILING DATE: 60/373,238  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 643  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-414-080-17

Query Match 93.9%; Score 3133.5; DB 4; Length 643;  
Best Local Similarity 92.4%; Pred. No. 1.5e-203;  
Matches 594; Conservative 10; Mismatches 22; Indels 17; Gaps 3;  
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Db 1 MFCVQAQYSPSPGSSYAAQYTSSEYTTBIMPDYTKLTMDLGSTTEITATATSLPSIST 60  
QY 61 FVEGSSNVELKPSVCYQMQQ----RPLIKVEGRAPSYHHHHHHHHHHHHHHHHHHHHHH 110  
Db 61 FMEGSSNVELKPSVCYQMQQGRPLIKVEGRAPSYHHHHHHHHHHHHHHHHHHHHHHHHHH 120  
QY 111 --OHCQPSIPASSPEDEVLPSTSMYFKQSPSTTTTTPAFPQAGALWDEALPSAPGCGIA 168

Db 121 PPQQQPSIPPPSGPEDEVLPSTSMYFKQSPSTTTTTPFPQAGALWDEALPSAQGCGIA 180  
QY 169 PGPILLDPPMKAVPTVAGARFPLFHFHFKPSPHPHPPAPSPAGGHHGLGYDPTAAAALSLPLG-- 226  
Db 181 PGPILLDPPMKAVPTVAGARFPLFHFHFKPSPHPHPPAPSPAGGHHGLGYDPTAAAALGLPLGAA 240  
QY 227 ---AAAAAGSQAALSHPHYGLPLAKRAAPLAPPLGLTPTSPASSLLGESPSLPSPSR 283  
Db 241 AAAAAAGSQAALSHPHYGLPLAKRAAALAFSPGLTPTSPASSLLGESPSLPSPSR 300  
QY 284 SSSSGEGTCVCGNNAACQHYGVRTCEGCKGFFKRTVQKNKYVCLANKNCVVKRRNR 343  
Db 301 STASGEGTCVCGNNAACQHYGVRTCEGCKGFFKRTVQKNKYVCLANKNCVVKRRNR 360  
QY 344 QYCRFQKCLSVGMVKEVVRTDSLGRRGRPLSPKPSPLQEPSPSPSPPICMNNALV 403  
Db 361 QYCRFQKCLSVGMVKEVVRTDSLGRRGRPLSPKPSPLQEPSPSPSPPICMNNALV 420  
QY 404 RALTDSTPRDLSDYRYCPTDQAAAGTDAEHVQOQFVNLTTASIDVSRSWAEKIPGFTDLPK 463  
Db 421 RALTDSTPRDLSDYRYCPTDQAAAGTDAEHVQOQFVNLTTASIDVSRSWAEKIPGFTDLPK 480  
QY 464 EDQTLLESFALEFLVLRSLRSNTAEDKFVFCNGLVLRQLRQCLRGFGEWLDISKDFSLN 523  
Db 481 EDQTLLESFALEFLVLRSLRSNTAEDKFVFCNGLVLRQLRQCLRGFGEWLDISKDFSLR 540  
QY 524 LQSLNLDIQALACLALSALSMITERHGLKEPKRVEELCNKITSSLDKHQSKGQALEPTESKV 583  
Db 541 LQSLNLDIQALACLALSALSMITERHGLKEPKRVEELCNKITSSLDKHQSKGQALEPTEPKV 600  
QY 584 LGALVELRKICTLGLQRIFYKLEDLVSPPSIIDKFLDITLPP 626  
Db 601 LRALVELRKICTLGLQRIFYKLEDLVSPPSIIDKFLDITLPP 643

RESULT 11  
US-10-755-889-64  
; Sequence 64, Application US/10755889  
; Publication No. US20040171823A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB  
; FILE REFERENCE: D0284 NP  
; CURRENT APPLICATION NUMBER: US/10/755,889  
; CURRENT FILING DATE: 2004-01-13  
; PRIOR APPLICATION NUMBER: U.S. 60/440,068  
; PRIOR FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: U.S. 60/469,757  
; PRIOR FILING DATE: 2003-05-12  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 64  
; LENGTH: 587  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-755-889-64

Query Match 93.6%; Score 3123; DB 4; Length 587;  
Best Local Similarity 99.8%; Pred. No. 7.1e-203;  
Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 40 MDLGSITEITATATSLPSISTFVEGSSNYELKPSVCYQMQRPLIKVEGRAPSYHHHHH 99  
Db 1 MDLGSITEITATATSLPSISTFVEGSSNYELKPSVCYQMQRPLIKVEGRAPSYHHHHH 60  
QY 100 HHH 159  
Db 61 HHH 120  
QY 160 LPSAPGCGIAPGLDPPPMKAVPTVAGARFPLFHFHFKPSPHPHPPAPSPAGGHHGLGYDPTAA 219





Db	179	MKAVPPMAAARFPPIF-FKSPPHPPAPSPAGGHHLYDPTAAALSLPLGAAAAAGSQA	237
QY	236	AALESHPYGLPLAKRAAPLAPPLGLTPSPTASSLLGESPSLPSPPSSSSSGEGTCAVC	295
Db	238	AALEGHYPGLPLAKRTATLTFPLGLTASPTASSLLGESPSLPSPPNRRSSSGEGTCAVC	297
QY	296	GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCFVDKRRNRRCQYCRFQKCLSV	355
Db	298	GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCFVDKRRNRRCQYCRFQKCLSV	357
QY	356	GMVKEVVRTDSLKGRGRRLPSKPKPLQOEPSQSPSPPICMNNAALVRALTDSTPRDLID	415
Db	358	GMVKEVVRTDSLKGRGRRLPSKPKPLQOEPSQSPSPPICMNNAALVRALTDSTPRDLID	417
QY	416	YSRYCPTDQAAAAGTDAEHVQOQFYNNLTASIDVSRGWAELKIPGFTDLPKEDQTLLESAPL	475
Db	418	YSRYCPTDQATAGTDAEHVQOQFYNNLTASIDVSRGWAELKIPGFTDLPKEDQTLLESAPL	477
QY	476	ELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGWLDISKDFSLNLQSLNLDIQALA	535
Db	478	ELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGWLDISKDFSLNLQSLNLDIQALA	537
QY	536	CLSALSMITERHGLKEPKRVEELCNKITSSSLKHOSKGOALBPTESKVLGALVELRKICT	595
Db	538	CLSALSMITERHGLKEPKRVEELCNKITSSSLKHOSKGOALBPTESKVLGALVELRKICT	597
QY	596	LGLQRIFYLKLLEDLVSPPSIIDKFLDLPF	626
Db	598	QGLQRIFYLKLLEDLVSPPSVIDKFLDLPF	628

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Job time : 76 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 17, 2006, 13:05:20 ; Search time 13 Seconds  
(without alignments)  
1378.302 Million cell updates/sec

Title: US-10-608-863-2

Perfect score: 3337,

Sequence: 1 MPCVQAQYSPSPGSSYAAQ.....EDLVSPPIIDKFLDITLPP 626

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*
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- 7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1745	52.3	598	US-11-198-640A-2	Sequence 2, Appli
2	533.5	16.0	533	US-11-124-368A-335	Sequence 335, App
3	479	14.4	435	US-11-166-412-62	Sequence 62, Appl
4	479	14.4	435	US-11-166-412-63	Sequence 63, Appl
5	479	14.4	458	US-11-166-412-61	Sequence 61, Appl
6	479	14.4	458	US-11-169-041-230	Sequence 230, App
7	411.5	12.3	541	US-11-118-855-26	Sequence 26, Appl
8	403.5	12.1	447	US-11-076-163-1	Sequence 1, Appli
9	403.5	12.1	447	US-11-166-412-52	Sequence 52, Appl
10	388	11.6	474	US-10-330-773-460	Sequence 460, App
11	388	11.6	480	US-10-330-773-457	Sequence 457, App
12	385	11.5	403	US-10-501-035-252	Sequence 252, App
13	382	11.4	457	US-10-330-773-462	Sequence 462, App
14	374	11.2	530	US-11-026-800-2	Sequence 2, Appli
15	368	11.0	460	US-11-076-163-5	Sequence 5, Appli
16	368	11.0	460	US-11-166-412-68	Sequence 68, Appl
17	359.5	10.8	477	US-11-156-272-9	Sequence 9, Appli
18	359	10.8	746	US-10-828-831-7	Sequence 7, Appli
19	357	10.7	1041	US-10-828-831-9	Sequence 9, Appli
20	355	10.6	579	US-10-501-035-317	Sequence 317, App
21	351.5	10.5	505	US-10-519-447-4	Sequence 4, Appli
22	349	10.5	845	US-11-094-519A-42	Sequence 42, Appl
23	345	10.3	837	US-11-094-519A-43	Sequence 43, Appl
24	337	10.1	746	US-10-828-831-5	Sequence 5, Appli
25	334.5	10.0	427	US-11-156-272-12	Sequence 12, Appl

#### ALIGNMENTS

##### RESULT 1

US-11-198-640A-2 450 7 US-11-156-272-10 Sequence 10, Appli  
 334.5 10.0 385 7 US-11-096-072A-3 Sequence 3, Appli  
 329 9.9 541 7 US-11-166-412-55 Sequence 55, Appli  
 326 9.8 385 7 US-11-096-072A-4 Sequence 4, Appli  
 324.5 9.7 495 7 US-11-166-412-54 Sequence 54, Appli  
 323.5 9.7 500 7 US-11-166-412-53 Sequence 53, Appli  
 318 9.5 777 6 US-10-658-986-4 Sequence 4, Appli  
 317 9.5 742 6 US-10-658-986-2 Sequence 2, Appli  
 34 231 306 7 US-11-166-412-220 Sequence 220, App  
 219 6.6 66 7 US-11-118-855-5 Sequence 5, Appli  
 217.5 6.5 688 7 US-11-106-674-1 Sequence 1, Appli  
 203.5 6.1 624 7 US-11-053-100-48 Sequence 48, Appli  
 203.5 6.1 774 7 US-11-053-100-49 Sequence 49, Appli  
 202 6.1 263 7 US-11-166-412-226 Sequence 226, App  
 198.5 5.9 241 6 US-10-993-143-14 Sequence 14, Appli  
 198.5 5.9 412 7 US-11-093-808-9 Sequence 9, Appli  
 198.5 5.9 412 7 US-11-093-808-11 Sequence 11, Appli  
 198.5 5.9 412 7 US-11-093-808-14 Sequence 14, Appli  
 198.5 5.9 775 7 US-11-053-100-51 Sequence 51, Appli  
 198.5 5.9 1225 7 US-11-053-100-50 Sequence 50, Appli

US-11-198-640A-2  
 ; Sequence 2, Application US/11198640A  
 ; Publication No. US20060040298A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmidt, Azriel  
 ; APPLICANT: Duong, Le Thi  
 ; APPLICANT: Pickaraki, Maureen  
 ; TITLE OF INVENTION: RHESUS MONKEY NURRI NUCLEAR RECEPTOR  
 ; FILE REFERENCE: 21228  
 ; CURRENT APPLICATION NUMBER: US/11/198,640A  
 ; CURRENT FILING DATE: 2005-08-05  
 ; PRIOR FILING DATE: 2004-08-05  
 ; NUMBER OF SEQ ID NOS: 17  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 598  
 ; TYPE: PRT  
 ; ORGANISM: Macaca mulatta  
 ; US-11-198-640A-2

Query Match 52.3%; Score 1745; DB 7; Length 598;  
 Best Local Similarity 54.4%; Pred. No. 5.3e-124;  
 Matches 362; Conservative 74; Mismatches 122; Indels 108; Gaps 18;

QY 1 MPCVQAQYSPSPGSSYAAQTY-----SSEYTTETWNPDDYTKLTMDLGSFETITATTTSIP 56  
 DB 1 MPCVQAQYSGSPQSGPASOSYSYHSGSXSDFLTPTPEFVKFMDLTNTEI--TATTSLP 58  
 QY 57 SITSFVSGYSNYELKPCSVYQW---ORPLIKVEGRAPSYHHHHHHHHHHHHHHHHQOH 112  
 DB 59 SFSTFMDNYSTGYDVKPPCLYQMLSCQSSIKVEDQMNYQOHSH----- 105  
 QY 113 QQPSIPPASSPEDEVLP-STSMYFKQSPPTPTTTFAPPPQAGALWDEALPAPGCIAPGP 171  
 DB 106 ---LPQS---EEMPHSGSVYKPSPPPTPTTTPGQVQHS PWDD-----PGS 148  
 QY 172 LLDPPMKAVPT-----VAGARFPLPHFKPSPHPPPA-----PSAPG 207  
 DB 149 LHNPHQNYVATTHMIEQKTPVSRLSLFSFKQSPPTFVSSCOMRFDFGLHPVMPNPEPAS 208  
 QY 208 GHILGYDPTAAALSLPLGAAAAGSQAALASHPYGLP-LAKRAAPLAPPLGLITPSP 266  
 DB 209 SHHW-----VDGQTFVAVNPDIRKPASMGFFGLQI---GH 239  
 QY 267 ASSILGSPSLPSPSPSSSSSGEGTCVCGDNAAACHYGVRTCEGCKGFFRTTVQKNKY 326

Db 240 ASQLL--DTQVSPBSRGSPSNEGLCAVCGDNAAQCHYGVRTCEGCKGFFKRTVQKNAY 297  
QY 327 VCLANKNCVDKRRNRNRCQYCFQKCLSVGMVKEVVRWTDLSKRRGRULPSKPSPLQOEP 386  
Db 298 VCLANKNCVDKRRNRNRCQYCFQKCLAVGMVKEVVRWTDLSKRRGRULPSKPSKPS-----P 352  
QY 387 SOPSPPSPICMNNALVRALTSTP--RDLDYSRY-CPDQAAAGTDAHVQOQFYNNLTA 443  
Db 353 QEPSPPSPVSLISALVRAHVDSNPAMTSLDYSRFOANPDYQMSGDDTQHIQOQFYDLTUG 412  
QY 444 STDVSRWAEKIPGFTDLPKEDQTLIESAFLELVLRSLRSNTAEDKFPVFCNGLVLRH 503  
Db 413 SNEIRGWAELPGADULPKADODLLFSAFLELVLRSLRSNTAEDKFPVFCNGLVLRH 472  
QY 504 LQCLRGFWLDSIKDPSNLQSLNDIOALACLALSMTIRHGLKPKRVEELCNKIT 563  
Db 473 LQCVRGFEWIDSIVEFSSNLQNMNIDISAFSCIAALAMVTERHGLKPKRVEELQNKIV 532  
QY 564 SSLKDHQ--SKQALQEPTE-SKVLGALVELRKICTLGLQRIEVLKLEDLVSPSIIDKLF 620  
Db 533 NCLKDHVTFNNGLNRPENYLSKLLKLPBLRTCTQGLQRIEVLKLEDLVPPPAIDKLF 592  
QY 621 LDTLPP 626  
Db 593 LDTLPP 598

## RESULT 2

US-11-124-368A-335  
; Sequence 335, Application US/11124368A  
; Publication No. US20050287559A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: James J. Devlin  
; APPLICANT: May Luke  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; Vascular Diseases, Methods of Detection and Uses Thereof  
; FILE REFERENCE: CL001524  
; CURRENT APPLICATION NUMBER: US/11/124,368A  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,845  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/625,936  
; PRIOR FILING DATE: 2004-11-09  
; NUMBER OF SEQ ID NOS: 21112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 335  
; LENGTH: 533  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-124-368A-335

Query Match 16.0%; Score 533.5; DB 7; Length 533;  
Best Local Similarity 29.7%; Pred. No. 1.1e-32;  
Matches 151; Conservative 70; Mismatches 189; Indels 99; Gaps 17;  
QY 118 PPASPEDEVLPSTMYFQSPSPSTPTTTPAFPPQAGALWDEALPSAPGCIAPGILLDPPM 177  
Db 83 PDSSSPNP--LP-----QGVPPSPPGPPLPSTA-----PSLGGSGAPP--PPM 124  
QY 178 KAVPTVAGARFPLFHEKPSPPHPPAPSPAGHHILGYDPTAAALSLPLGAAAAGSQAAA 237  
Db 125 P--PPPLGSPFPVSSSMGSGLPFPAPPFGPGFVSSPOINSTVSLPFGGSG----- 174  
QY 238 LESHYPGLPLAKRAAPLAPFPPLGLTSPSTASSLGSPLSPSPSSSGEGTCAVCGD 297  
Db 175 -----PPEDVKP-----PVLVGRGLHCPPPPGPGAGKELCAICGD 210  
QY 298 NAACQHYGVRTCEGCKGFFKRTVQKNAYKVCVLANKNCPVDKRRNRNRCQYCFQKCLSVGM 357  
Db 211 RSSGKHGYVCEGCKGFFKRTIRKDLTYSRDNKDCVTDKQRNRCQYCRYQKCLATGM 270  
QY 358 VKEVVRTSLKGRGRULPSKPSPLQOEPSPSPSPICMNNALVRALTSTP----- 406

Db 271 KREAVQBERQRG-----KKQDG-DGEGAGAEEMVDRILELAELAEVQKSDQGVGP 322  
QY 407 -----TSTPRDLDSRYCPTDQAAAGTDAHVQOQFYNNLTFASIDVSRWAEKIPGFTDL 461  
Db 323 GGTGGSGSPND-----PVTNICQAAD-----KQLFTLV-----EWAKRIPIHFSSL 363  
QY 462 PKEDQTLIESAFLELVLRSLRSNTAEDKFPVFCNGLVLRHLCQ-LRGFGEWLDLSI-KD 519  
Db 364 PLDDQVILLRAGWNEILLIASFSHRSIDVRDGIILLATGLHVRNSAHSAGVAIFORVLTE 423  
QY 520 FSLNLQSLNDIOALACLALSMTIRHGLKPKRVEELCNKITSSLKDH--OSKQOALE 577  
Db 424 LVSKMRDRMRDKTELGCURLIILFNPDKAGLSNFSSEVLEKRVKTASLETYCKQKYPQO 483  
QY 578 PTESKVLGALVELRKICTLGLQRIEVLKLE 606  
Db 484 GRFAKLLRLPALRSIGUKLEHLFFPKL 512

## RESULT 3

US-11-166-412-62  
; Sequence 412, Application US/11166412  
; Publication No. US20060014231A1  
; GENERAL INFORMATION:  
; APPLICANT: Van Rompaey, Luc  
; APPLICANT: Tomme, Peter H. M.  
; TITLE OF INVENTION: Methods and Compositions To Promote Bone Homeostasis  
; FILE REFERENCE: P27,927-D USA  
; CURRENT APPLICATION NUMBER: US/11/166,412  
; CURRENT FILING DATE: 2005-06-24  
; PRIOR APPLICATION NUMBER: 60/582,704  
; PRIOR FILING DATE: 2004-06-24  
; PRIOR APPLICATION NUMBER: 60/630,449  
; PRIOR FILING DATE: 2004-11-23  
; PRIOR APPLICATION NUMBER: 60/673,206  
; PRIOR FILING DATE: 2005-04-20  
; NUMBER OF SEQ ID NOS: 231  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 62  
; LENGTH: 435  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-166-412-62

Query Match 14.4%; Score 479; DB 7; Length 435;  
Best Local Similarity 29.7%; Pred. No. 1.1e-28;  
Matches 136; Conservative 76; Mismatches 176; Indels 70; Gaps 13;  
QY 194 KPSPHPPAPSPAGHHILGYDPTAAALSLPLGAAAAGSQAAALSHHPYGLPLAKRAAP 253  
Db 17 KTEPSPASLTDSVNH-----SPGSSDASGSYSSTNMGHQGLD----- 57  
QY 254 LAFPPPLGLTPSTASSLGSPE-----SLPSPSSSSSGEGT 291  
Db 58 --SPPL-----YSPAPILGSGFVRKLYDDCSSTIVEDPQTKCEYMLNSMPK-----L 104  
QY 292 CAVCGDNAAQCHYGVRTCEGCKGFFKRTVQKNAYKVCVLANKNCPVDKRRNRNRCQYCFQK 351  
Db 105 CLVCGDIASGYHYGVASCEACKAFPKRTIQNIEYSCPATNECEITKRRRSQACRFMK 164  
QY 352 CLSVGMVKEVVRTSLKGRGRULPSKPSPLQOEP-SOPSPPSPICMNNALVRALTST 410  
Db 165 CLKVGMLEGVRLDRVRG--GRQYKRRIDAENSPLYNPQLVQPAKKYKYNKISHLVAE 222  
QY 411 PRDLDSRYCPTDQAAAGTDAHVQOQFYNNLTFASIDVSRWAEKIPGFTDLPKEDQTLI 470  
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QY 471 ESAFLELVLRSLRSNTAEDKFPVFCNGLVLRHLCQ-LRGFGEWLDLSI-KDPSNLQSLNL 529  
Db 279 QSANMEILLGVVVRSLSFEDVLVYADDYIMDEQSKLAGLLDLNNAIQLVKKYKSMKL 338



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 17, 2006, 22:16:03 ; Search time 635 Seconds  
(without alignments)  
10620.581 Million cell updates/sec

Title: US-10-608-863-1  
Perfect score: 3794  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 130357 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents\_NA.\*

- 1: /cgn2\_6/ptodata/1/ina/1-COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5-COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A-COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B-COMB.seq.\*
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- 6: /cgn2\_6/ptodata/1/ina/PCTUS-COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/ina/PP-COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/ina/RE-COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3779.4	99.6	3797	3	US-09-949-016-3789
2	3722	98.1	3802	3	US-09-949-016-905
3	2689.6	70.9	2714	3	US-09-023-655-928
4	1420.4	37.4	47184	3	US-09-949-016-12647
5	1420.4	37.4	47184	3	US-09-949-016-15531
6	497	13.1	3427	3	US-09-023-655-1400
7	497	13.1	3427	3	US-09-949-016-828
8	497	13.1	3427	3	US-09-949-016-4467
9	486.4	12.8	1797	3	US-09-277-078-1
10	418.4	11.0	690	3	US-10-131-827-8211
11	363.8	9.6	2486	3	US-09-949-016-4392
12	340.6	9.0	2637	3	US-09-566-921-58
13	315.6	8.3	601	3	US-09-949-016-35444
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19	135.6	3.6	601	3	US-09-949-016-135226
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22	109.6	2.9	2538	3	US-09-949-016-5701
23	109.4	2.9	1245	2	US-09-132-619-3
24	109.4	2.9	1245	3	US-09-282-803B-3

ALIGNMENTS

RESULT 1

US-09-949-016-3789  
; Sequence 3789, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3789  
; LENGTH: 3797  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-3789

Query Match 99.6%; Score 3779.4; DB 3; Length 3797;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 3793; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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Qy	61	CCGCGCCCCCACCCTCCAGTCTCTGCTCTCTCTCCGCTCCCATACACAGCGGCTCA	120
Db	61	CCGCGCCCCCACCCTCCAGTCTCTGCTCTCTCTCCGCTCCCATACACAGCGGCTCA	120
Qy	121	CACCGCT	180
Db	121	CACCGCT	180
Qy	181	TTGCT	240
Db	181	TTGCT	240
Qy	241	CCGCGCTGAGCGCCCTCCCGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	300
Db	241	CCGCGCTGAGCGCCCTCCCGGCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	300

Ds	241	CGCAGCTGGACGCCCTCCCGGGCTCACTTTGCAACGCTGACGCTGGCGGACGTGGCGG	300
Qy	301	TGGAGGTGGGAACAGCGCGGCAATCCTCCCGCTGGTCAAGCCCAAGCAGGACGCCCG	360
Ds	301	TGGAGGTGGGAACAGCGCGGCAATCCTCCCGCTGGTCAAGCCCAAGCAGGACGCCCG	360
Qy	361	CGGAACCTCTCGGCTGTCTCTCCATGAGTCGGATCGCAGCATCCCGCCACCGCGCT	420
Ds	361	CGGAACCTCTCGGCTGTCTCTCCATGAGTCGGATCGCAGCATCCCGCCACCGCGCT	420
Qy	421	CACCGCTCCGCGAGCCGCTGGGCTTGTAACCGCAGCGCTTCGCGGACAGCAGCTGTGA	480
Ds	421	CACCGCTCCGCGAGCCGCTGGGCTTGTAACCGCAGCGCTTCGCGGACAGCAGCTGTGA	480
Qy	481	CTCCCCCAGTGCAGATTTTGGGACAGCTCTCTAGAAATCTGCTTTAAAGACGGAAACG	540
Ds	481	CTCCCCCAGTGCAGATTTTGGGACAGCTCTCTAGAAATCTGCTTTAAAGACGGAAACG	540
Qy	541	CCACAGCACTCAAGCCCACTCGCGAAGGCGAGCGCCGCGCAAGCCCGGCGCTGAGCCT	600
Ds	541	CCACAGCACTCAAGCCCACTCGCGAAGGCGAGCGCCGCGCAAGCCCGGCGCTGAGCCT	600
Qy	601	GGACCTTTAGCGGTGCGCGGAGCACTGCGCGGCTTCGCTCGCGGAGCGTCCGCTCCT	660
Ds	601	GGACCTTTAGCGGTGCGCGGAGCACTGCGCGGCTTCGCTCGCGGAGCGTCCGCTCCT	660
Qy	661	CCTACACTCTCAGCTTCGCTGGAGAGACCCCGCCCAACATTCAGCGGCGAAGATAC	720
Ds	661	CCTACACTCTCAGCTTCGCTGGAGAGACCCCGCCCAACATTCAGCGGCGAAGATAC	720
Qy	721	CCTCCAGATATGCCCTGGTCCAGGCCAATATAGCCCTTCCCTCCAGGTTCCAGTTAT	780
Ds	721	CCTCCAGATATGCCCTGGTCCAGGCCAATATAGCCCTTCCCTCCAGGTTCCAGTTAT	780
Qy	781	GGGGCGCAGACATACAGCTCGGAATACACCGAGATCATGAACCCCGCATACACCAAG	840
Ds	781	GGGGCGCAGACATACAGCTCGGAATACACCGAGATCATGAACCCCGCATACACCAAG	840
Qy	841	CTGACCATGGAACCTTTGGAGCACTGAGATTCAGGCTACAGCCCAACGCTCCCGCAGC	900
Ds	841	CTGACCATGGAACCTTTGGAGCACTGAGATTCAGGCTACAGCCCAACGCTCCCGCAGC	900
Qy	901	ATCAGTACTCTCGTGGAGGCTCTCGAGCACTACGAACTTCCCTGCGGTGAC	960
Ds	901	ATCAGTACTCTCGTGGAGGCTCTCGAGCACTACGAACTTCCCTGCGGTGAC	960
Qy	961	CAAAATGACGCGCCCTTGATCAAAAGTGGAGGCGGCGCGCCAGCTTACCATCACCAT	1020
Ds	961	CAAAATGACGCGCCCTTGATCAAAAGTGGAGGCGGCGCGCCAGCTTACCATCACCAT	1020
Qy	1021	CACCAACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAT	1080
Ds	1021	CACCAACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAT	1080
Qy	1081	CCTCCAGCTCCAGCCCGGAGACGAGTGTGCCCCAGACCTCCATGACTTCAAGCAG	1140
Ds	1081	CCTCCAGCTCCAGCCCGGAGACGAGTGTGCCCCAGACCTCCATGACTTCAAGCAG	1140
Qy	1141	TCCCCACCGCTCCAGCCCGGAGACGAGTGTGCCCCAGACCTCCATGACTTCAAGCAG	1200
Ds	1141	TCCCCACCGCTCCAGCCCGGAGACGAGTGTGCCCCAGACCTCCATGACTTCAAGCAG	1200
Qy	1201	GAGGCACTGCGCTCGGCGCGCGCTGCAATCGCAACCGCGCGCTGCGGACCGCGGATG	1260
Ds	1201	GAGGCACTGCGCTCGGCGCGCGCTGCAATCGCAACCGCGCGCTGCGGACCGCGGATG	1260
Qy	1261	AGGCGGTCCCAACCGTGGCGCGCTTCCGCTCTTCCATCTCAAGCCCTCGCGG	1320
Ds	1261	AGGCGGTCCCAACCGTGGCGCGCTTCCGCTCTTCCATCTCAAGCCCTCGCGG	1320
Qy	1321	CGGCATCCCCCG	1380
Ds	1321	CGGCATCCCCCG	1380
Qy	1381	GCTCCCGGCTCAGCCTGCGCTGGAGCGCGCAGCGCGCGCGCGCGCGCGCGCGCGCG	1440
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Qy	1441	CTTCAGAGCCACCGTACGGGCTCGCTGCGCAAGAGGGCGCGCGCGCTTCGCGTTCGCG	1500
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Ds	1501	CCTCTCGGCTCAGCGCTCCCTTACCGCGTCCAGCTGCTGGCGGAGAGTCCAGCGCTG	1560
Qy	1561	CGCTCGCGCCCGCAGCAGAGCTCGTCTGCGCAGGCGCAGTGTGCGTGTGGGGAC	1620
Ds	1561	CGCTCGCGCCCGCAGCAGAGCTCGTCTGCGCAGGCGCAGTGTGCGTGTGGGGAC	1620
Qy	1621	AACCGCGCTGCGCAGCACTACGGCGTGAACCTTCGAGGGCTGCAAGGGCTTTTCAAG	1680
Ds	1621	AACCGCGCTGCGCAGCACTACGGCGTGAACCTTCGAGGGCTGCAAGGGCTTTTCAAG	1680
Qy	1681	AGAACAGTGCAGAAAAATGCAAAATATGTTTTCCTGCGCAAAATAAAACTGCCAGTAGAC	1740
Ds	1681	AGAACAGTGCAGAAAAATGCAAAATATGTTTTCCTGCGCAAAATAAAACTGCCAGTAGAC	1740
Qy	1741	AAGAGAGTGCAGAACCGATGTCAGTACTGTCGATTTCAAGATGCTCAGTGTGGAATG	1800
Ds	1741	AAGAGAGTGCAGAACCGATGTCAGTACTGTCGATTTCAAGATGCTCAGTGTGGAATG	1800
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Ds	1801	GTAAGAGAGTGTTCGCTACAGATAGTCTGAAGGGAGGAGGTGCTGCTCCCTTCCAAA	1860
Qy	1861	CAAAGAGCCCATTAACAACAGGAACTTCTCAGCCCTTCCACCTTCTCCTCCAATCTGC	1920
Ds	1861	CAAAGAGCCCATTAACAACAGGAACTTCTCAGCCCTTCCACCTTCTCCTCCAATCTGC	1920
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Qy	1981	AGATACTGTCCCACTGACCGGCTGCTGAGGCAAGATGCTGAGCATGTGCAAAATTC	2040
Ds	1981	AGATACTGTCCCACTGACCGGCTGCTGAGGCAAGATGCTGAGCATGTGCAAAATTC	2040
Qy	2041	TACAACTCTGACAGCGCTCCATTTGATGTATCCAGAGCTGGGAGAGAAAGATTCGGGA	2100
Ds	2041	TACAACTCTGACAGCGCTCCATTTGATGTATCCAGAGCTGGGAGAGAAAGATTCGGGA	2100
Qy	2101	TTTACTGATCTCCCAAGAGATCAGACATTAATTGATCAGCCCTTTTGGAGCTG	2160
Ds	2101	TTTACTGATCTCCCAAGAGATCAGACATTAATTGATCAGCCCTTTTGGAGCTG	2160
Qy	2161	TTTGTCTCAGACTTTCCATCAGGTCAAACTGCTGAAGATAAGTTGTGTTCTGCAAT	2220
Ds	2161	TTTGTCTCAGACTTTCCATCAGGTCAAACTGCTGAAGATAAGTTGTGTTCTGCAAT	2220
Qy	2221	GGACTTGTCTGCAATGCACTTTCACTGCTGAGATTTGGGAGTGGCTGACTCTATT	2280
Ds	2221	GGACTTGTCTGCAATGCACTTTCACTGCTGAGATTTGGGAGTGGCTGACTCTATT	2280
Qy	2281	AAAGACTTTTCTTAAATTTTCAGAGCTGAACTTGTATATCCAGCCTTTAGCCTGCTG	2340
Ds	2281	AAAGACTTTTCTTAAATTTTCAGAGCTGAACTTGTATATCCAGCCTTTAGCCTGCTG	2340
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Ds	2341	TCAGCACTGACATGATCACAAGAAAGATGCGGTAAAGAAACCAAGAGAGTCCGAAG	2400
Qy	2401	CTATGCAACAGATCACAAGCAGTTTAAAGACCAACAGAGTAAAGGACAGGCTCTGGAG	2460
Ds	2401	CTATGCAACAGATCACAAGCAGTTTAAAGACCAACAGAGTAAAGGACAGGCTCTGGAG	2460

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Db 3061 GCTTCTGTATCAAGGTACGTATGTGTGCAACAGGAGAACTTCTTTTAAATTC 3120
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## RESULT 2

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US-09-949-016-905
; Sequence 905, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 905
; LENGTH: 3802
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-905
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Query Match 98.1%; Score 3722; DB 3; Length 3802;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 3779; Conservative 0; Mismatches 15; Indels 8; Gaps 4;
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3059	Qy	ATGCTTCCTGTATCAAAAGTACGTATCTGTGTGCAACAAAGCCAGAAACTTCCCTTTAAT	3118
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3179	Qy	GGCAAAACAAATATAGTGTGTTTGTCCATAAACAAGTGCAATTTTTTAAAGTGCTGTCT	3238
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3301	Db	TGTTAGCAAAATGACACGTAAATATCCCTACGAGGCTGTGTTTACCTTCCCTGTGCGATC	3360
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3361	Db	CCTTCTGAGGTATGGCCCATCCAAGACTTTTAGGCCATTTCTGATGAAACCGATCCCTG	3420
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3421	Db	CCCTGACTGTCCAGCTATCTGAAAGTGGATCAGATTATATAACTGATTCATGTAACGTG	3480
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3539	Qy	TGACTGTGATATTCAATTCAGAAGCGCCATAAGTCAGTTGAGTATTTTATCCCTAGATAAG	3598
3541	Db	TGACTGTGATATTCAATTCAGAAGCGCCATAAGTCAGTTGAGTATTTTATCCCTAGATAAG	3600
3599	Qy	AACATGCAAAATCAGCAGGAACCTGGTCATACAGGGTAAAGCAACAGGACAAATAGGATTTT	3658
3601	Db	AACATGCAAAATCAGCAGGAACCTGGTCATACAGGGTAAAGCAACAGGACAAATAGGATTTT	3660

Qy	3659	TATAGATATAAATTAAATTTTTTGGTTA--TTCGTTAAGGAGA-CAAATTTTGGAGAGCAAGCA	3715
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Qy	3716	AA---TCCTTTTTAAAAATAGTAGTAATGTGAATACTAGAAAAGATTTAAAAAATAGTAT	3772
Db	3721	AATCTTCTTTTTAAAAAATAGTAGTAATGTGAATACTAGAAAAGATTTAAAGAAATAGTAT	3780
Qy	3773	GAGTGTGAGTACTAGGAAGGAT	3794
Db	3781	GAGTGTGAGTACTAGGAAGGAT	3802

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RESULT 3
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; Sequence 928, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION O
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 928:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2714 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1311504
US-09-023-655-928

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	% Matches 2692;	Conservative	0;	Mismatches	4; Indels
					0; Gaps
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Db	19	TCACAAACACACACACACAAAGCGCGCACACAGGCTCCGCACACACACTTCGCTCTCCC			78
QY	192	GCSCGGCTCACACCCCTCTTGCCTTGTGAGCCCTTGCCTGTCAGCGCGCGCGCAGCTGGA			251

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Db 139 GCGCCCTCCCGGGCTCACTTTGCAACGTGACGGTGGCGGCGAGTGGCGGTGAGGTGGGA 198  
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Db 259 GGCTGTGTCTCCCATGAGTCGGGATCGCAGATCCCGCACCGCGCTCAACCGCTCCG 318  
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; Sequence 12647, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTRI, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12647
; LENGTH: 47184
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12647

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Matches 1434; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

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QY 44347 TGGGGAATCCAAATATAGTTGCTTTGATTTTAAAAAAGAACAGCCAGGGTTGTCG 44406
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QY 44407 CAGGTAGGATGTGCTTTAAAGATTGGTCTCTGAAAAATATGCTTCTGTTTCAAGGTA 44466
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QY 44467 CGTATGCTGCAAAACAAGGAGAACTTCTTTTAAATTTCTTCTTCTTCTTAACT 44526
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QY 44527 AAATGCTGAAAGATGGAGGATTTACTCAAAATCAGACATGCAAAACATATGCTGTT 44586
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QY 44587 TGCTTCCATAAACCAAGTGCAATTTTAAAGTGCTGCTTAAAGTCTTCTGTTTAACT 44646
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QY 44647 TCTCTTTTATTTCTATATGGAATATAAAGGAGGAGGAGTCAATGTTAGCAAAATGACAGTTAA 44706
QY 3320 TATCCCTAGCAGAGGCTGTGTTTCACTTCCCTGTCGATCCCTTCTGAGGTATGCCCATC 3379
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QY 44707 TATCCCTAGCAGAGGCTGTGTTTCACTTCCCTGTCGATCCCTTCTGAGGTATGCCCATC 44766
QY 3380 CAAGACTTTTAGGCCATTTCTGATGGAACAGATCCCTGCTGCTGCTGCTGCTGCTGCT 3439
Db |||||
QY 44767 CAAGACTTTTAGGCCATTTCTGATGGAACAGATCCCTGCTGCTGCTGCTGCTGCTGCT 44826
QY 3440 GAAAGTCGATCAGATTATAAATCTGGATTACATGTAATGTTTGGTGTGTTCTATCAAC 3499
Db |||||
QY 44827 GAAAGTCGATCAGATTATAAATCTGGATTACATGTAATGTTTGGTGTGTTCTATCAAC 44886
QY 3500 CCACACAGAGTTCCTTAAACTTGTTCAGTTATAGTAACTGACCTGCTGCTGCTGCTGCTGCT 3559
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QY 44887 CCACACAGAGTTCCTTAAACTTGTTCAGTTATAGTAACTGACCTGCTGCTGCTGCTGCTGCT 44946
QY 3560 AGCCCAATAGTCAAGTTGAGTATTGATCCCTAGATAAGAACATGCAAAATCAGCAGGAAC 3619
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QY 44947 AGCCCAATAGTCAAGTTGAGTATTGATCCCTAGATAAGAACATGCAAAATCAGCAGGAAC 45006
QY 3620 TGGTCATACAGGGTAAGCAACAGGGAACAATAAGGATTTTATAGATATAATTTATTTT 3679
Db |||||
QY 45007 TGGTCATACAGGGTAAGCAACAGGGAACAATAAGGATTTTATAGATATAATTTATTTT 45066
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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3794	100.0	3794	8	US-10-608-863-1	Sequence 1, Appli
2	3792	98.1	3802	3	US-09-853-386-46	Sequence 46, Appl
3	3722	98.1	3802	3	US-09-853-386-78	Sequence 78, Appl
4	3722	98.1	3802	6	US-10-414-080-1	Sequence 1, Appl
5	3732	98.1	3802	8	US-10-659-004-115	Sequence 115, App
6	3679.2	97.0	5828	6	US-10-247-671-105	Sequence 105, App
7	3668.2	96.7	5842	5	US-10-002-600-53	Sequence 53, Appl
8	2875	75.8	4977	3	US-09-873-367C-229	Sequence 239, App
9	2875	75.8	4977	7	US-10-755-889-63	Sequence 63, Appl
10	2875	75.8	4977	9	US-10-843-641A-229	Sequence 229, App
11	2689.6	70.9	2714	7	US-10-641-643-928	Sequence 928, App
12	2500	65.9	4400	3	US-09-853-386-47	Sequence 47, Appl
13	2500	65.9	4400	5	US-10-003-169-3	Sequence 3, Appli
14	2500	65.9	4400	6	US-10-414-080-2	Sequence 2, Appli
15	2500	65.9	4400	7	US-10-191-803-209	Sequence 209, App
16	2371	62.5	5115	3	US-09-853-386-57	Sequence 57, Appl
17	2371	62.5	5115	6	US-10-414-080-8	Sequence 8, Appli
18	1485.6	39.2	1884	3	US-09-853-386-62	Sequence 62, Appl
19	1485.6	39.2	1884	5	US-10-005-169-1	Sequence 1, Appli
20	1022.8	27.0	1606	3	US-09-853-386-55	Sequence 55, Appl
21	1022.8	27.0	1606	6	US-10-414-080-6	Sequence 6, Appli
22	553.2	14.6	600	10	US-11-060-756-1816	Sequence 1816, Ap
23	553.2	14.6	600	10	US-11-060-756-6088	Sequence 6088, Ap

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90  
80  
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60  
50  
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30  
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10  
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Tot

	Query Match	100.0%;	Score 3794;	DB 8;	Length 3794;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 3794;	Conservative	0;	Mismatches	0;
				Indels	Gaps
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Db	1	ATAAATGACGTGCCGAGAGACGAGCGAAGCGCAGCGCGGAGACGGAGTCTCTCGCT	60		
Qy	61	CCCGCCCCCACCCTCCAGTCTCTGCTCTCTCCGCTCCCATACACAGACGGGTCA	120		
Db	61	CCCGCCCCCACCCTCCAGTCTCTGCTCTCTCCGCTCCCATACACAGACGGGTCA	120		
Qy	121	CACCGGTCTCCTCACTCGACACACAGACACAGACGGCGGCACACAGGTCCGCACACAC	180		
Db	121	CACCGGTCTCCTCACTCGACACACAGACACAGACGGCGGCACACAGGTCCGCACACAC	180		
Qy	181	TTCCGCTCTCCCGCGCGGTACACACCCCTCTTTGCCCTGAGCCCTTTGCCGTTGCAGCGCGCG	240		

Db 181 TTGCTCTCCCGCGCTCACACCCCTCTTGCCCTGAGCCCTTGCCGCTGACGCGCGC 240  
Qy 241 CCGAGCTGGAGCGCCCTCCCGGGCTCACTTTGCAACGCTGACGGTGC CGGCAGTGGCG 300  
Db 241 CCGAGCTGGAGCGCCCTCCCGGGCTCACTTTGCAACGCTGACGGTGC CGGCAGTGGCG 300  
Qy 301 TGGAGGTGGGAACAGCGCGCATCTCCCTCCCTGGTCACAGCCCAAGCCAGGAGCGCCG 360  
Db 301 TGGAGGTGGGAACAGCGCGCATCTCCCTCCCTGGTCACAGCCCAAGCCAGGAGCGCCG 360  
Qy 361 CGGAACCTCTCGGCTGTGCTCTCTCCATGAGTGGGATCGCAGCATCCCCACCAAGCGCT 420  
Db 361 CGGAACCTCTCGGCTGTGCTCTCTCCATGAGTGGGATCGCAGCATCCCCACCAAGCGCT 420  
Qy 421 CACCGCTTCGGGAGCCGTGGCTTTGACACCGAGCCCTTCGGGAGCAGAGCTGTGA 480  
Db 421 CACCGCTTCGGGAGCCGTGGCTTTGACACCGAGCCCTTCGGGAGCAGAGCTGTGA 480  
Qy 481 CTCCTCCCGAGTGCAGATTTGGGAGAGCTCTCTAGAACTCGCTCTAAAGACGGAACCG 540  
Db 481 CTCCTCCCGAGTGCAGATTTGGGAGAGCTCTCTAGAACTCGCTCTAAAGACGGAACCG 540  
Qy 541 CCACAGCACTCAAAGCCCACTGCGGAAGAGGCGAGCCCGCAAGCCCGGGCCCTGAGCCT 600  
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Qy 601 GGACCTTAGCGGTGCGGGGAGCACTGCGGGCGCTTCGCCCTGCGGAGCTCGCTCCT 660  
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Db 721 CTTCCAGATATGCCCTGCTGCTCCAGCCCAATATAGCCCTTCGCCCTCCAGGTTTCAAGTTAT 780  
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Db 781 GGGGCGAGACATACAGCTCGGAATACACCGAGAGATCATGAACCCCGACTACACCAAG 840  
Qy 841 CTGACCATGGACCTTTGGCAGCACTGAGATCAGCGCTACAGCCACCACTGCTGCCCGCAGC 900  
Db 841 CTGACCATGGACCTTTGGCAGCACTGAGATCAGCGCTACAGCCACCACTGCTGCCCGCAGC 900  
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Qy 1141 TCCCAACCGTCAACCCCAACCAACCGCGCTTCGCCCGCAGGCGGGCGGTATGGGAC 1200  
Db 1141 TCCCAACCGTCAACCCCAACCAACCGCGCTTCGCCCGCAGGCGGGCGGTATGGGAC 1200  
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Db 1201 GAGGCACTGCCCTCGGCGCGGCTGATCGCACCCGCGCGCTGCTGACCCCGCGATG 1260  
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Qy 1681 AGAAGCTGCAAGAAATGCAAAATATGTTGCTGCGCAATAAACTGCCAGTAGAC 1740  
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Qy 1741 AAGAGCTCGAAACCGATGTCAGTCTGTCGATTTAGAAAGTCTCAGTGTGGAAATG 1800  
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Qy 1801 GTAAAAGAGTGTGTCGTA CAGATAGTCTGAAAAGGAGAGAGTGTGCTGCTTCCAAA 1860  
Db 1801 GTAAAAGAGTGTGTCGTA CAGATAGTCTGAAAAGGAGAGAGTGTGCTGCTTCCAAA 1860  
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1379 CGGCTGCCGCTCAGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1438

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1381 CCGCTCGCGGCTCAGCTGCGCTGGAGCGCGCAGCGCGCGCGCGGCGAGCCAGCGCGCG 1440  
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Db  
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QY  
1979 CCAGATCTGTCCACTGACCGAGCTGTGAGGACAGATGCTGAGCATGTGCAACAT 2038  
Db  
1981 CCAGATCTGTCCACTGACCGAGCTGTGAGGACAGATGCTGAGCATGTGCAACAT 2040  
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2221 ATGACTTGTCTGATCGACTTTCAGTCTTCTGTTGATTTGGGAGTGGCTCGACTCTA 2280  
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2459 AGCCACCGAGTCCAGGTTCTGGGTGCTGTTAGAACTGAGGAGAGTCTGCAACCTGG 2518  
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2461 AACCCACGAGTCCAGGTTCTGGGTGCTGTTAGAACTGAGGAGAGTCTGCAACCTGG 2520



Qy	419	CTCACC	CGCTCC	CGGAG	CGCGTGG	CTTGTAT	CACCCG	CAGCCCTT	CCGGG	CACGAGCTGT	478
Db	421	CTCACC	CGCTCC	CGGAG	CGCGTGG	CTTGTAT	CACCCG	CAGCCCTT	CCGGG	CACGAGCTGT	480
Qy	479	GACTCC	CCCCAG	TGACAG	TTTCGG	GACAGCTCT	CTAGAA	CTCGCTCT	TAAG	ACCGGAAC	538
Db	481	GACTCC	CCCCAG	TGACAG	TTTCGG	GACAGCTCT	CTAGAA	CTCGCTCT	TAAG	ACCGGAAC	540
Qy	539	CGCCAC	CAGCACTCAA	AGCCCACTCG	CGAAGAGG	GACGCCG	CGAAGCCCG	GGCCCTTG	AGC		598
Db	541	CGCCAC	CAGCACTCAA	AGCCCACTCG	CGAAGAGG	GACGCCG	CGAAGCCCG	GGCCCTTG	AGC		600
Qy	599	CTGGAC	CCCTTAG	CGGTG	CCGGG	CAGCACTGC	CGCGCTT	CCCTTC	CGCCG	ACGTCGCTC	658
Db	601	CTGGAC	CCCTTAG	CGGTG	CCGGG	CAGCACTGC	CGCGCTT	CCCTTC	CGCCG	ACGTCGCTC	660
Qy	659	CTCCTA	CACCTCTAG	CCCTCG	CTGGAG	AGCCCCC	CAGCCCA	CAATTC	CAGGCG	CAAGAT	718
Db	661	CTCCTA	CACCTCTAG	CCCTCG	CTGGAG	AGCCCCC	CAGCCCA	CAATTC	CAGGCG	CAAGAT	720
Qy	719	ACCCCT	CCAGATAT	GCCCTG	CGTCCA	AGCCCAATAG	CCCTT	CCCTTC	CCAGG	TTCCAGTT	778
Db	721	ACCCCT	CCAGATAT	GCCCTG	CGTCCA	AGCCCAATAG	CCCTT	CCCTTC	CCAGG	TTCCAGTT	780
Qy	779	ATCGGG	CGCAGACAT	ACAGCT	TCGGAATAC	CACCGAGATCAT	GAACCC	CCGACT	TACACCA		838
Db	781	ATCGGG	CGCAGACAT	ACAGCT	TCGGAATAC	CACCGAGATCAT	GAACCC	CCGACT	TACACCA		840
Qy	839	AGCTGAC	ATGGACTTTG	GGAGCACTG	AGATCA	CGGCTAC	AGCCAC	CACAGCT	CCCTG	CCCA	898
Db	841	AGCTGAC	ATGGACTTTG	GGAGCACTG	AGATCA	CGGCTAC	AGCCAC	CACAGCT	CCCTG	CCCA	900
Qy	899	GCATCAG	TACCTTCGT	GAGGGCTACT	CGAGCAACT	ACGAACCT	CAAGCCTT	CCCTG	CGCTGT		958
Db	901	GCATCAG	TACCTTCGT	GAGGGCTACT	CGAGCAACT	ACGAACCT	CAAGCCTT	CCCTG	CGCTGT		960
Qy	959	ACCAAA	TGACGCGCCCTT	GTATCAA	AGTGGAG	GGGGCG	CGCCAG	CTACCAT	CACC		1018
Db	961	ACCAAA	TGACGCGCCCTT	GTATCAA	AGTGGAG	GGGGCG	CGCCAG	CTACCAT	CACC		1020
Qy	1019	ATGACCA	CCACCA	CCACCA	CCACCA	CCATAT	CCAGCAG	CAGCAT	CAGCAG	CCATCCA	1078
Db	1021	ATGACCA	CCACCA	CCACCA	CCACCA	CCATAT	CCAGCAG	CAGCAT	CAGCAG	CCATCCA	1080
Qy	1079	TTCTCT	CCAGCTCC	CAGCCCG	GAGACAG	AGTGCTGCC	CAGCACCT	CCATGT	TACTTA	CAAGC	1138
Db	1081	TTCTCT	CCAGCTCC	CAGCCCG	GAGACAG	AGTGCTGCC	CAGCACCT	CCATGT	TACTTA	CAAGC	1140
Qy	1139	AGTCCCC	ACCGTCCA	CCCCCA	CCAGCG	CGCTTTCCCC	CCCGCAG	CGGGG	CGTAT	TGGG	1198
Db	1141	AGTCCCC	ACCGTCCA	CCCCCA	CCAGCG	CGCTTTCCCC	CCCGCAG	CGGGG	CGTAT	TGGG	1200
Qy	1199	ACGAGG	CACCTG	CGCGCC	CGGCTG	CATCG	CACCGG	CCCGCT	GCTGGA	CCCGCGGA	1258
Db	1201	ACGAGG	CACCTG	CGCGCC	CGGCTG	CATCG	CACCGG	CCCGCT	GCTGGA	CCCGCGGA	1260
Qy	1259	TGAAGG	GGGTCCC	CACG	GTGCG	CGCTTTCC	CGCTTCC	CACTTCA	AGCCCT	TCG	1318
Db	1261	TGAAGG	GGGTCCC	CACG	GTGCG	CGCTTTCC	CGCTTCC	CACTTCA	AGCCCT	TCG	1320
Qy	1319	CGCCG	CATCCCC	CGCCAG	CCCGG	CGCGCC	ACCACT	TCGGT	TACG	ACCCGACG	1378
Db	1321	CGCCG	CATCCCC	CGCCAG	CCCGG	CGCGCC	ACCACT	TCGGT	TACG	ACCCGACG	1380
Qy	1379	CGCTG	CGCGCT	CAGCCT	GCTGG	AGCCG	CAGCGG	CGG	CAGCC	AGCGCGG	1438
Db	1381	CGCTG	CGCGCT	CAGCCT	GCTGG	AGCCG	CAGCGG	CGG	CAGCC	AGCGCGG	1440
Qy	1439	CGCTTT	GAGG	ACAC	CCGT	TACG	GGCTCG	CGCTGG	CCAG	AGGGCGG	1498
Db	1441	CGCTTT	GAGG	ACAC	CCGT	TACG	GGCTCG	CGCTGG	CCAG	AGGGCGG	1500
Qy	1499	CGCCT	CTCG	GGCT	CTCAC	GCCTT	CCCTAC	CGGCT	CCAG	CTGCTGGG	1558

1501	Db	CGCCTCTCGGCCTTCAGCCCTCCCTACCGGCTCGACGCTGCTGGCGAGAGTCCAGCC	1561
1559	Qy	TGCGGTGCGCGCCACGAGAGCTCGTCTGCTGGCGAGGCGACGTGTGCCGTGTGCGGGG	1618
1561	Db	TGCGGTGCGCGCCACGAGAGCTCGTCTGCTGGCGAGGCGACGTGTGCCGTGTGCGGGG	1620
1619	Qy	ACAACCGCGCTGCCAGCACTACGGCGTGGAAACCTGCGAGGGCTCGAAGGCTTTTTCA	1678
1621	Db	ACAACCGCGCTGCCAGCACTACGGCGTGGAAACCTGCGAGGGCTCGAAGGCTTTTTCA	1680
1679	Qy	AGAGACAGTGCAGAAAAATGCAAAATATGTTTGCCTGGCAAAATAAAACCTGCCAGTAG	1738
1681	Db	AGAGACAGTGCAGAAAAATGCAAAATATGTTTGCCTGGCAAAATAAAACCTGCCAGTAG	1740
1739	Qy	ACAAGAGAGCTGCAAAACCGATGTCAGTACTGTCGATTTTCAAGAGTGTCTCAGTGTGGAA	1798
1741	Db	ACAAGAGAGCTGCAAAACCGATGTCAGTACTGTCGATTTTCAAGAGTGTCTCAGTGTGGAA	1800
1799	Qy	TGTTAAAGAGTTGTCCGTACAGATAGTCTGAAAGGAGAGAGGTGCTGCTCCATCT	1858
1801	Db	TGTTAAAGAGTTGTCCGTACAGATAGTCTGAAAGGAGAGAGGTGCTGCTCCATCT	1860
1859	Qy	AACCAAAGAGCCATTACAAACAGGAACCTTCTCAGCCCTCTCCACCTTCTCCTCCATCT	1918
1861	Db	AACCAAAGAGCCATTACAAACAGGAACCTTCTCAGCCCTCTCCACCTTCTCCTCCATCT	1920
1919	Qy	GCATGATGAAATGCTTGTCCGAGCTTTAACACACTCAACACCCAGAGATCTTGATTATT	1978
1921	Db	GCATGATGAAATGCTTGTCCGAGCTTTAACACACTCAACACCCAGAGATCTTGATTATT	1980
1979	Qy	CCAGATACTCTCCACTGACAGGCTGCTGACGCGACAGATGCTGAGCATGTGCAACAAT	2038
1981	Db	CCAGATACTCTCCACTGACAGGCTGCTGACGCGACAGATGCTGAGCATGTGCAACAAT	2040
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2041	Db	TCTAACACTCTGACAGCCCTCATTTGATGATTCAGAGCTGGCGAGAAAGATTCGG	2100
2099	Qy	GATTTACTGATCTCCCAAAGAGATCAGACATTTACTTTTGAATCAGCCCTTTTGGAGC	2158
2101	Db	GATTTACTGATCTCCCAAAGAGATCAGACATTTACTTTTGAATCAGCCCTTTTGGAGC	2160
2159	Qy	TGTTTGTCTCAGACTTTCCATCAGGTCAACACTGCTGAAGATAAGTTGTGTCTGCA	2218
2161	Db	TGTTTGTCTCAGACTTTCCATCAGGTCAACACTGCTGAAGATAAGTTGTGTCTGCA	2220
2219	Qy	ATGGACTTGTCTCGATCGACTTCAGTGCCTTCGTGGAATTTGGGAGTGCTCGACTCTA	2278
2221	Db	ATGGACTTGTCTCGATCGACTTCAGTGCCTTCGTGGAATTTGGGAGTGCTCGACTCTA	2280
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2339	Qy	TGTCAGCACTGAGCATGATCACAGAAAGACATGGGTTTAAAGAACCAAGAGAGTCGAAG	2398
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2399	Qy	AGCTATGCAACAGATCACAAAGAGTTTAAAGACACACAGAGTAAGGGAACAGGCTCTGG	2458
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2459	Qy	AGCCCAACGAGTCCAGGTCCTGGTGCCCTGGTGTAGAACTGAGGAAGATCTGCACCTGG	2518
2461	Db	AACCAACGAGTCCAGGTCCTGGTGCCCTGGTGTAGAACTGAGGAAGATCTGCACCTGG	2520
2519	Qy	GCCTCCAGCGCATCTTACCTGAAGCTGGAAGACTTTGGTGTCTCCACCTTCCATCATTTG	2578
2521	Db	GCCTCCAGCGCATCTTACCTGAAGCTGGAAGACTTTGGTGTCTCCACCTTCCATCATTTG	2580
2579	Qy	ACAAGCTTCTCTGGAACCCCTACCTTTCTAATCAGGAGCAGTGGAGCAGTGAGCTGCCT	2638



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Qy 2819 TTATATTAGGATTTGGGGATGGGTGGAGGGGTTATAGTTTCATGAGGGTTTCTAA 2878  
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Db 3181 GGCAAAACAAATAGCTGTTTGCCTTCCATAAACAAGTGCAATTTTTTAAAGTGTCT 3240  
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Qy 3659 TATAGATATAATTTAAATTTTGTGA--TTGTTTAAAGAGA--CAATTTTGGAGCAAGCA 3715  
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## RESULT 4

US-10-414-080-1  
; Sequence 1, Application US/10414080  
; Publication No. US20030220288A1  
; GENERAL INFORMATION:  
; APPLICANT: MULLICAN, SHANNON E.  
; APPLICANT: MILBRANDT, JEFFREY  
; TITLE OF INVENTION: NOR-1 AND NUR77 NUCLEAR RECEPTORS AS TARGETS FOR  
; FILE REFERENCE: P02454US1  
; CURRENT APPLICATION NUMBER: US/10/414,080  
; PRIOR FILING DATE: 2003-04-15  
; PRIOR APPLICATION NUMBER: 60/373,238  
; PRIOR FILING DATE: 2002-04-17  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-414-080-1

Query Match 98.1%; Score 3722; DB 6; Length 3802;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 3779; Conservative 0; Mismatches 15; Indels 8; Gaps 4;

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Qy 121 CACCGCTCCTCTACTCGGACACACAGACACAAAGCGGCGCACAGGCTCCGACACAC 178  
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Qy 179 ACTTCGCTCTCCGCGGCTCACACCCCTCTTGCCTTGGCCCTGAGCCCTTGGCGGTGACGCGG 238  
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Qy 299 CGTGAGGTGGGAACAGCGGCGGATCCTCCCTCTGGTCAAGCCCAAGCAGGACGCC 358  
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Qy 359 CGCGGAACCTCTCGGCTGTGCTCTCCATGAGTGGGATCGCAGCATCCCCCAGCGG 418  
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Qy 419 CTCAACGCTCTCCGCGGAGCGCTGGGCTTGTACACCGCAGCGCTTCCGCGGACAGCAGTGT 478  
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Qy 479 GACTCCCCCAGTGCAGATTTTGGGACAGCTCTTAGAAAATCGCTCTTAAAGCGGAAC 538  
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RESULT 5

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US-10-659-004-115
; Sequence 115, Application US/10659004
; Publication No. US20050048507A1
; GENERAL INFORMATION:
; APPLICANT: Zhong et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-608
; CURRENT APPLICATION NUMBER: US/10/659,004
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/295,607
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/295,661
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/296,404
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/296,418
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/297,414
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/297,567
; PRIOR FILING DATE: 2001-06-12
; PRIOR APPLICATION NUMBER: 60/298,285
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/298,556
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/299,949
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/300,883
; PRIOR FILING DATE: 2001-06-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 115
; LENGTH: 3802
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (732)..(2609)
US-10-659-004-115
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Query Match 98.1%; Score 3722; DB 8; Length 3802;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 3779; Conservative 0; Mismatches 15; Indels 8; Gaps 4;

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Db 61 CCGCGCCCCACCCCTCCAGCTCCTGCTCCTCCTCCGCTCCCATACACAGACGCGTCA 120
Qy 121 CACCCGCTCCTCTACTCGACACACACAGACAGCGCGGACACAGGCTCCG--CACAC 178
Db 121 CACCCGCTCCTCTACTCGAAACACACACAGACAGCGCGGACACAGGCTCCGACAC 180
Qy 179 ACTTTCGCTCTCCGCGGCTCACACCCCTCTTCCCTGAGCCCTTCCGCTGAGCGCG 238
Db 181 ACTTTCGCTCTCCGCGGCTCACACCCCTCTTCCCTGAGCCCTTCCGCTGAGCGCG 240
Qy 239 CGCGCAGCTGGAGCGCCCTCCCGGGCTCACTTTGCAACGCTGACGCTGCCGCGAGTGC 298
Db 241 CGCGCAGCTGGAGCGCCCTCCCGGGCTCACTTTGCAACGCTGACGCTGCCGCGAGTGC 300
Qy 299 CGTGGAGGTGGGAACAGCGCGCGGATCTCTCCCTCTGGTCAACAGCCCAAGCAGGAC 358
Db 301 CGTGGAGGTGGGAACAGCGCGCGGATCTCTCCCTCTGGTCAACAGCCCAAGCAGGAC 360
Qy 359 CGCGGAACCTCTCGGCTGTCTCTCCATGAGTCGGGATCGCAGCATCCCCCAGCGCG 418
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Db 361 CGCGGAACTCTCGGTGTGCTCTCCATGAGTCGGGATCGAGCATCCCCACAGCGG 420  
QY 419 CTCACGGCTCCGGAGCGCTGGCTTGTATACCGCAGCCCTTCGGGACAGCAGCTGT 478  
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QY 479 GACTCCCCCAGTGCAGATTTTCGGGACAGCTCTCTAGNAATCTGCTCTAAAGACGGAA 538  
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QY 539 CGCCACAGCACTCAAAGCCCACTGCGGAAGAGGGCAGCCCGGCAAGCCCGGCCCTGAGC 598  
Db 541 CGCGACAGCACTCAAAGCCCACTGCGGAAGAGGGCAGCCCGGCAAGCCCGGCCCTGAGC 600  
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Db 1501 CGCTCTCGGCTTACGGCTTCCCTACCGGCTCAGGCTGCTGGGCGAGAGTCCCGACC 1560  
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Db 1801 TGGTAAAGAGGTTGTCCGTACAGATAGTCTGAAAGGAGGAGAGGTCGCTGCGCTTCCA 1860  
QY 1859 AACCAAGAGGCCATTAACAAGGAACTTCTCAGCCCTTCCAACCTTCTCCTCAATCT 1918  
Db 1861 AACCAAGAGGCCATTAACAAGGAACTTCTCAGCCCTTCCAACCTTCTCCTCAATCT 1920  
QY 1919 GCATGATGAATGCTTGTGTCGAGCTTTAAACAGACTCAACACCCAGAGATCTTGATTA 1978  
Db 1921 GCATGATGAATGCTTGTGTCGAGCTTTAAACAGACTCAACACCCAGAGATCTTGATTA 1980  
QY 1979 CCAGATAGTGTCCCACTGACAGGCTGCTGAGGACACAGATGCTGAGCATGTGCAACA 2038  
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QY 2039 TCTACACCTCCTGAGAGCTTCCATTTGATGATTCAGAGCTGGGAGAGAAAGATTCGG 2098  
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QY 2099 GATTTACTGATCTCCCAAGAGATCAGACATTTATTGAAATCAGCCCTTTTGGAGC 2158  
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QY 2159 TGTGTGCTCAGACTTTTCCAATCAGGTCAAACTGCTGAAAGATAAGTTGTGTTCTCA 2218  
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QY 2577 TGACAAAGCTCTTCTGACACACCTTCTTAATCAGAGCAGTGGAGCAGTGAAGTGC 2636  
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QY 3057 ATATGCTCTCTGTTATCAAGGTAGTATGCTGCAACAGGAGGAGAACTTCCTTTTAA 3116  
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Db 3781 AGTGTGAGTACTAGCAAGGAT 3801

RESULT 7

US-10-002-600-53  
; Sequence 53, Application US/10002600  
; Publication No. US2002013707A1  
; GENERAL INFORMATION:  
; APPLICANT: Hopkins, Christopher M.  
; APPLICANT: Peterson, David P.  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Hawkins, Phillip R.  
; TITLE OF INVENTION: GENES REGULATED IN ACTIVATED T-CELLS  
; FILE REFERENCE: PA-0042 US  
; CURRENT APPLICATION NUMBER: US/10/002,600  
; PRIOR FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: 60/243,521  
; PRIOR FILING DATE: 2000-10-25  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PERL Program  
; SEQ ID NO 53  
; LENGTH: 5642  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Template ID: 349343.3  
; NAME/KEY: unsure  
; LOCATION: 1012-1074, 4045-4075  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-002-600-53

Query Match 96.7%; Score 3668.2; DB 5; Length 5642;  
Best Local Similarity 98.1%; Pred. No. 0;

Matches 3728; Conservative 0; Mismatches 56; Indels 8; Gaps 5;

QY 1 ATAAATGACGTGCGAGAGAGCGAGCGAAGCGCAGCGCGGAGAGCGAGTCTCTGCT 60  
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QY 299 CGTGGAGGTGGGAAACAGCGCGCGCATCTCTCCCTCTGCTCTCTCTCTCTCTCTCTCT 358  
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QY 359 CGCGGAACTCTCTCGGCTGTCTCTCCATGAGTGGGATCGCAGCATCCCCCACCAGCG 418  
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Db 2941 ATATAACTGTTTAAACCTTCTTGGGAATCCAAATTATAGTCTCTTGTATTTAAAA 3000
Qy 2996 CAAGAACAGCAAGGGTGTTCGCGAGGTAGGTGCTTAAAGATTGGTCCCTGAA 3055
Db 3001 CAAGAACAGCAAGGGTGTTCGCGAGGTAGGTGCTTAAAGATTGGTCCCTGAA 3060
Qy 3056 AATATGCTTCTGTATCAAGAGTATGTTGGTCAACAAAGGACAGAACTTCTCTTTA 3115
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Qy 3656 TTTTATAGATATAATTTTATTTTGTATTTAGGTTAAGGAGACAAATTTGGAGACCAAGCA 3715
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Qy 3773 GAGTGTGAGTACTAGGAAGGAT 3794
Db 3781 GAGTGTGAGTACTAGGAAGGAT 3802
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## RESULT 8

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US-09-873-367C-229
; Sequence 229, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endress, Gregory
; APPLICANT: Augustus, Meena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE OF INVENTION: Signature Gene Sets
; CURRENT APPLICATION NUMBER: US/09/873,367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236,842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244,867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245,084
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 229
; LENGTH: 4977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-229
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Query Match 75.8%; Score 2875; DB 3; Length 4977;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 40; Indels 19; Gaps 9;
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Qy 791 CATACAGCTCGGAATACACACGAGATCATGAACCCCGACTACACAGCTGACCATGG 850
Db 154 CATACAGCTCGGAATACACACGAGATCATGAACCCCGACTACACAGCTGACCATGG 213
Qy 851 ACCTTGGCAGCCTGAGATCAGGCTACAGCCACGCTCCCTCCAGCATCAGTACT 910
Db 214 ACCTTGGCAGCCTGAGATCAGGCTACAGCCACGCTCCCTCCAGCATCAGTACT 273
Qy 911 TCGTGGAGGGCTACTCGAGCAACTACGAACCTCAAGCCCTTCTGCTGTGTACCAATGCGAGC 970
Db 274 TTGTGGAGGGCTACTCGAGCAACTACGAACCTCAAGCCCTTCTGCTGTGTACCAATGCGAGC 333
Qy 971 GGCCCTTGATCAAGTGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1030
Db 334 GGCCCTTGATCAAGTGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 393
Qy 1031 ACCAACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1090
Db 394 ACCAACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 453
Qy 1091 CCAGCCCGAGGAGGAGGTGCTGCCAGCACCTTCCCTCCTAGTACTTCAAGCAGTCCCAACCGT 1150
Db 454 CCAGCCCGAGGAGGAGGTGCTGCCAGCACCTTCCCTCCTAGTACTTCAAGCAGTCCCAACCGT 513
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QY 1151 CCACCCCAACGCGCGGCTTCCCGCCGACGCGGGGGCGTTATGGAGCGAGGCACTGC 1210  
Db 514 CCACCCCAACGCGCGGCTTCCCGCCGACGCGGGGGCGTTATGGAGCGAGGCACTGC 573  
QY 1211 CCTCGGCGCGGCTGCACTCGACCCGCGCGCTCTGACCCCGCGGATGAAGGCGGTCC 1270  
Db 574 CCTCGGCGCGGCTGCACTCGACCCGCGCGCTCTGACCCCGCGGATGAAGGCGGTCC 633  
QY 1271 CCACGGTGGCGGCGCGGCTTCCCGCTTCCACTTCAAGCCCTCGCGCGCATCCCC 1330  
Db 634 CCACGGTGGCGGCGCGGCTTCCCGCTTCCACTTCAAGCCCTCGCGCGCATCCCC 693  
QY 1331 CGCGCCCAAGCCCGCGCGGCGGCAACCACTCGGCTACGACCGGACGCGGCTCGCGCG 1390  
Db 694 CGCGCCCAAGCCCGCGCGGCGGCAACCACTCGGCTACGACCGGACGCGGCTCGCGCG 753  
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Qy 3788 GAAGGAT 3794  
Db 3140 GAAGGAT 3146

## RESULT 9

US-10-755-889-63  
; Sequence 63, Application US/10755889  
; Publication No. US20040171823A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB  
; FILE OF INVENTION: PATHWAY  
; FILE REFERENCE: D0284 NP  
; CURRENT APPLICATION NUMBER: US/10/755,889  
; CURRENT FILING DATE: 2004-01-13  
; PRIOR APPLICATION NUMBER: U.S. 60/440,068  
; PRIOR FILING DATE: 2003-01-14  
; PRIOR APPLICATION NUMBER: U.S. 60/469,757  
; PRIOR FILING DATE: 2003-05-12  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 63  
; LENGTH: 4977  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-755-889-63

Query Match 75.8%; Score 2875; DB 7; Length 4977;  
Best Local Similarity 98.1%; Pred. No. 0;  
Matches 3008; Conservative 0; Mismatches 40; Indels 19; Gaps 9;  
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Db	1354	CCACTGACCAGGCTGCTGCAGGCACAGATGCTGAGCATGTGCACAAATTTCTACAACCTCC	1413
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Qy	2171	GACTTTCCATCAGGTCAAACACTGCTCGAAGATAAGTTGTGTCTGCAATGGACTTTGTCTC	2230
Db	1534	GACTTTCCATCAGGTCAAACACTGCTCGAAGATAAGTTGTGTCTGCAATGGACTTTGTCTC	1593
Qy	2231	TGCATCGACTTCAGTGCTCGTGATTTGGGGAGTGGCTCGACTCTATTAAAGACTTTT	2290
Db	1594	TGCATCGACTTCAGTGCTCGTGATTTGGGGAGTGGCTCGACTCTATTAAAGACTTTT	1653
Qy	2291	CCTTAAATTTGCAGAGCCTGAAACCTTGATATCCNAGCCTTAGCCTGCCTGTGAGCACTGA	2350
Db	1654	CCTTAAATTTGCAGAGCCTGAAACCTTGATATCCNAGCCTTAGCCTGCCTGTGAGCACTGA	1713
Qy	2351	GCATGATCAGAAAGACATGGGTTTAAAGAAACCAAGAGAGCTCGAAGACTATGCAACA	2410
Db	1714	GCATGATCAGAAAGACATGGGTTTAAAGAAACCAAGAGAGCTCGAAGACTATGCAACA	1773
Qy	2411	AGATCACAAAGCAGTTTAAAGACCAACAGAGTAAGGGACAGGCTCTGGAGCCCAACCGAGT	2470
Db	1774	AGATCACAAAGCAGTTTAAAGACCAACAGAGTAAGGGACAGGCTCTGGAGCCCAACCGAGT	1833
Qy	2471	CCAAGTCTCGGGTGCCTTGGTAGAACTGAGGAAGATCTGCAACCTGGGCTCCAGGGCA	2530
Db	1834	CCAAGTCTCGGGTGCCTTGGTAGAACTGAGGAAGATCTGCAACCTGGGCTCCAGGGCA	1893
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Db	1894	TCCTTCTACCTGGAAGCTGGAAGACTTGGTGTCTCCACCTTCATCATTTGACAAAGCTCTTC	1953
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Qy	2651	CCTGCTGTCTACGAGCAAAAGGGATAGGTTTGGAAAACCTATFATCTTCTGTCTCTCTTA	2710
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Db	2194	ATTGGGGATGGGTGGAGGGGTTATAGTTCATGAGGGTTTCTAAGAAATTCCTTAAC	2253
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Db	2254	AAAGCACTTTTGGCAATGCTATCCAGCAGGAAAAGGATAATTAACCTGTTTTAA	2313
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Qy	3011	GTTGTTGCGCCAGGGTAGGATGTCTTAAAGATTTGGTCCCTTGAAAAATATGCTTCTGTGA	3070
Db	2374	GTTGTTGCGCCAGGGTAGGATGTCTTAAAGATTTGGTCCCTTGAAAAATATGCTTCTGTGA	2433

QY	3071	TCAAAGTACGTATGGTGCAGAAACAAGGCAGAAACCTTCTTTTAAATTTCCCTTCTCTTCCCTT	3133
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DB	2494	TATTTTAAACAATGGTCAAGAGTGGAGGATTA	2551
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DB	2609	T---TATACTCTCTTATCTATATATGCGGAAATAAAAAAGGAGGAGCAGTCATGTTAGCAAAATG	2665
QY	3311	ACAGCTTAATATCCCTAGCAGAGCTGTGTTACACCTTCCCTGTCGATCCCTTCTGAGGTA	3370
DB	2666	ACAGCTTAATATCCCTAGCAGAGCTGTGTTACACCTTCCCTGTCGATCCCTTCTGAGGTA	2725
QY	3371	TGGCCCATCCAAGACTTTTAGGCCATCTCTTGTAGGAACAGATCCCTGCGCCTGACTGTCC	3430
DB	2726	TGGCCCATCCAAGACTTTTAGGCCATCTCTTGTAGGAACAGATCCCTGCGCCTGACTGTCC	2785
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DB	2905	TCATTCAGAGCGCCATAAGTCAGTTCAGTATTTTGATCCCTAGATAAGAACATGCAAAATC	2959
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QY	3671	TTAATTTTGTATATGGTTAAGGAGACAATTTGGAGAGCAGCAAAA---TCCTTTTAAA	3727
DB	3020	TTAATTTTGTATATGGTTAAGGAGACAATTTGGAGAGCAGCAAAA---TCCTTTTAAA	3079
QY	3728	AAATAGTATGAATCGTAATCTAGAAAGATTTTAAAAATAGTATGAGTGAGTACTAG	3787
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RESULT 10			
US-10-843-641A-229			
; Sequence 229, Application US/10843641A			
; Publication No. US2005006454A1			
; GENERAL INFORMATION:			
; APPLICANT: Avalon Pharmaceuticals, Inc.			
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using			
; FILE OF INVENTION: Signature Gene Sets			
; FILE REFERENCE: 689290-189			
; CURRENT APPLICATION NUMBER: US/10/843,641A			
; CURRENT FILING DATE: 2004-05-12			
; PRIOR APPLICATION NUMBER: US/09/873,367			
; PRIOR FILING DATE: 2001-06-05			
; PRIOR APPLICATION NUMBER: US/09/954,531			
; PRIOR FILING DATE: 2001-09-18			
; PRIOR APPLICATION NUMBER: US/09/954,456			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US/09/962,436			
; PRIOR FILING DATE: 2001-09-25			
; PRIOR APPLICATION NUMBER: US/09/962,832			

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; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 229
; LENGTH: 4977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-229

Query Match      75.8%; Score 2875; DB 9; Length 4977;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 3008; Conservative 0; Mismatches 40; Indels 19; Gaps 9;

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DB 154 CATACAGCTCGGAATACACCGAGAGATCATGAACCCGAGCTACACCAAGCTGACATGG 213
QY 851 ACCTTGGCAGCACTGAGATCAGGCTCAGCCACCAACCTCCCTGCGGAGCATCAGTACT 910
DB 214 ACCTTGGCAGCACTGAGATCAGGCTCAGCCACCAACCTCCCTGCGGAGCATCAGTACT 273
QY 911 TCGTGGAGGGCTACTCGAGCACTACGAACCTTCAAGCCTTCTGCGGTACCAAAATGACG 970
DB 274 TTGTGGAGGGCTACTCGAGCACTACGAACCTTCAAGCCTTCTGCGGTACCAAAATGACG 333
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## RESULT 11

US-10-641-643-928  
; Sequence 928, Application US/10641643  
; Publication No. US20040077003A1  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; Susan G. Stuart  
; Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
; GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/641,643  
; FILING DATE: 14-Aug-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 928:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2714 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: q1311504  
; SEQUENCE DESCRIPTION: SEQ ID NO: 928 :  
US-10-641-643-928

Query Match 70.9%; Score 2689.6; DB 7; Length 2714;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2692; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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3291 AGTCATGTTATCAACCGGCTGCTCATTTTCTTAGCTCACCCCTTGGTCCACTGCGCTGT 3350  
3354 CGATCCCTTCTGAGGTATGGCCCATCCAAAGCTTTTATAGGCCATTTCTGATGGAACAGAT 3413  
3351 AGAACCTTCCGAGGTATGGCCCTTCTAAGACTTTTCAAGGCACTTTGATGGAATTCGAC 3410  
3414 CCC-----TGCCCTGACTGTGCGAGCTATCCCTGAAAGTGCATGAGATTAATACTG 3463  
3411 ACCCTCCCTCAACCCATGACTATCCAGATGTCCTGAATGGGATCAGGTTATAAATG 3470  
3464 GATTACATGTAACCTGTTTGGTTGTTGTT-TCTATCAACCCCAAGAGTTCCTTAAACTTG 3522  
3471 GATTGCAATGACTGTGTTGCTGTGTTGTTGTTCAACCTGGACAGAGTCTCTTAAACCTT 3530  
3523 CTTTCAGTTATAGTAACTGACTGTTGTTATATTCATTCAAGAGC-----GCCATAAGTCACT 3575  
3531 CTTTAGTTGTAGCAAGTTCCTGATTCCTCCATTCCAGAGCCCAAGGAGCATTTGGTGACT 3590  
3576 TGAGTATTTGATCCCTAGATAAGAACATGCAATTCAGCAGGAACT-GGTCTATACAGGTA 3634  
3591 CGATCAAGGGTTAACCCCTAGGAGAACATGCAATAAGTGAAGTGGGTTCAGACAGGTA 3650  
3635 AGCACCGGACATAAGGATTTTATAGATAT-----AATTTAATTTTGTATTGG 3687







Db	1674	CGCAAAATATGTTTCTCTGGCAATAAATAACCTGCCCCGTGACACAGAGACGTGCAAAATCG	1733
Qy	1758	ATGTCAGTACTGTCTGATTTTCAGAAAGTGTCTCAGTGTTCGAAATGTAAGAAAGTGTGTCGG	1817
Db	1734	ATGTCAGTACTGCAGGTTTCAGAAAGTGTCTCAGTGTGGGATGCTGAAGAAAGTGTGTCGG	1793
Qy	1818	TACAGATAGTCTGAAGGGAGGAGAGTGTCTGCTGCTTCCAAACCAAGAGGCCCATTAACA	1877
Db	1794	TACAGATAGTCTGAAGGGAGGAGAGTGTCTGCTTCCAAACCAAGAGGCCCATTAACA	1853
Qy	1878	ACAGGAACCTTCTCAGCCCTCTCCACCTTCTCTCCATCTGCGATGATGAATGCCCTGT	1937
Db	1854	ACAGGAGCCCTGCGAGCCCTCCACCAATCTCTCCGATCTGTATGATGAACGCCCTGT	1913
Qy	1938	CCGAGCTTTAAACAGACTCAACACCCAGAGACTTGATTTATTCAGATACTGTCCCACTGA	1997
Db	1914	CCGAGCTTTAAACAGAGCAACGCCAGAGACTTGATTTATTCAGATACTGTCCCACTGA	1973
Qy	1998	CCAGGCTGCTGAGGCAAGATGCTGAGCATGTGCAACAAATTCACAACTCTCTGACAGC	2058
Db	1974	CCAGGCCACTCGGGGCAAGAGCTGTGAGCAAGTGCAGCAGTCTTACAACTTCTGACGGC	2033
Qy	2058	CTCCATTGATGCTATCCAGAACTCGGCAAGAAAGATTCCGGGATTTACTGATCTCCCAA	2117
Db	2034	CTCCATGACGTGTCCAGAACTGGGCAAGAAAGATCCCGGATTCATGATCTCCCAA	2093
Qy	2118	AGAAATCAGACATTTACTTTATTTGAATCAGCCCTTTTGGAGCTGTTGTCTCAGACTTTC	2177
Db	2094	AGAAATCAGAGCTTACTTTATAGAAATCAGCCCTTTTGGAGCTGTTGTCTTAGACTTTC	2153
Qy	2178	CATCAGGTCAAACTCTGCTGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCTCTGCAATCG	2237
Db	2154	TATCAGGTCAAACTCTGCTGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCTCTGCAATCG	2213
Qy	2238	ACTTCAGTGCCTTCGTGATTTGGGAGTGTGCTCGACTCTATTAAAGACTTTTCTTTAAA	2297
Db	2214	ACTTCAGTGCCTTCGTGATTTGGGAGTGTGCTCGACTCTATTAAAGACTTTTCTTTAAA	2273
Qy	2298	TTTGCAGAGCCCTGAACTTTGATATCCAAAGCCCTTAGCCCTGCTGTGACACTGTAGCATGAT	2357
Db	2274	TTTGCAGAGCCCTGAACTTTGATATCCAAAGCCCTTAGCCCTGCTGTGACACTGTAGCATGAT	2333
Qy	2358	CACAGAAGACATGGGTTAAAGAAACCAAGAGAGTCCGAAGACTATGCAACCAAGATCAC	2417
Db	2334	CACAGAGCGACATGGGTTAAAGAAACCAAGAGAGTGGAGAGCTATGCAACCAAGATCAC	2393
Qy	2418	AAGCAGTTTAAAGACCAACAGAGTAGAGGACAGGCTCTGGAGCCCAACGAGTCCAAAGT	2477
Db	2394	AAGCAGTTTAAAGACCAACAGAGTAGAGGACAGGCTCTGGAGCCCAACGAGTCCAAAGT	2453
Qy	2478	CCTGGGTGCCCTGGTGTAGAACTGAGGAAGATCTGCACCCCTGGGCTCTCAGCGCATCTTCTA	2537
Db	2454	CCTTCGGCACTGTGTGAACTGAGGAAGATCTGCACCCAGGGCTCTCAGCGTATCTTCTA	2513
Qy	2538	CCTGAAGCTGGAACACTGTGTGTCTCAACCTTCCATATTGCAAGCTCTTCTCTGGACAC	2597
Db	2514	CCTGAAGCTGTGAGACTTGTGTGTCTCCACCTTCTGTGTCATGCAAGCTCTTCTCTGTATC	2573
Qy	2598	CCTACCTTTCTAATCAGAGCAG-TGAGCAGTAGAGTGTGCTCTCTCTTAGCACCTGTCT	2656
Db	2574	CCTGCCCTTTCTGACACGGGAAGCCTGAGCAGAGAGCTACTTGTCTCTGCTGGCACCTGGTC	2633
Qy	2657	TGCTACGCAGCAAAAGGATAGTTTGGAAACCTATCATTTTCTGTCTCTTCTTAAGAGGA	2716
Db	2634	ATTAAGTGAAGCAAAAGATGGTTTGAACACT-GCCCTCTTATCTCTTCTCCAGGGGAA	2692
Qy	2717	AAAGCAGCTCTCTGTAGAAGCAAAAGACTTTCTTTTTTTTCTGTGCTCTTTTCTTACAACC	2776
Db	2693	AAAGCAGCTCCATAGAAGCAAAAGACTTT-TTTTTTTCTGTGCACTTTTCTTACAACC	2751
Qy	2777	TAAAGCAGAAAACTTCGACAGTATTTGTGTGGGTTGTGTTTATATTTAGGCAATGGG	2836
Db	2752	TAAAGCAGAAAACTTCGACAGTATTTGTGTGGGTTGTGTTTATATTTAGGCTTTGGT	2811

QY	2837	GGATGGGGTGGGAGGGGGT--TATAGTTTCATGAGGGTTTTCTAAGAAATTCGTAACAAAG	2899
DB	2812	GGGTGGGCTGGGAGGGGGTAAAAAGTTCATGAGGCTTTTCTAAGAAATTCGTCACGAAG	2871
QY	2895	CACTTTTGGCAATGCTATCCACGAG-----GMAAAAAAGATATAATACTGTTTT	2948
DB	2872	CACTTTTGGATGATCTATCCAGCAGTGGGTGGGGAAGGATATATATCTGTTTT	2931
QY	2949	AAAA--CTCTTTCTGGGGAATCCAAATPATATGTTGCTTTGTATTTAAAAACAAGAACGCC	3006
DB	2932	AAAAACTCTTTCCGGGGGAATAGCTATGCTTATGTTTGTGTTTATTTAAAAATAAGAACGCC	2991
QY	3007	AAGGGTTG-TTCGCCAGGATAGGATGTCTTAAAGATTGGTCCTTGAATAATATGCTTC	3065
DB	2992	AAGGGCTGTTTTTACCAAGGTAGGGCTGTGCTTTAAGACTGATCCCTTAGTAGTGTACTTC	3051
QY	3066	CTGTATCAAAAGGTACGTATGTGGTGGCAACAAGGCAGAAA-----CTTCCTTT	3113
DB	3052	CCGATC-GAGGCACATAGTGTGCAATGAGCGGGGGAATCTTCAATTCCTCATTT	3110
QY	3114	TAATTTCTTCTTCTTTATTTTAAACAAATGGTGAAGATGGAGGATTACTACAANTCA	3173
DB	3111	CTTTCCTTCTTTAAAAATAAATGGCAAAAAAAGATGGAAGATTCTACAANTCA	3170
QY	3174	GACATGCCAAAACAATATGGCTGTGTTCCTTCATATAACAAGTGCAATTTTTTAAAGTGC	3233
DB	3171	GACTTAGCAAAATGATAATGGCTATTGCTTTCACATACAAGTGCAATTTTTTAGAGTGC	3230
QY	3234	TGCTTACTAAGTCTGTTTTATTAACCTCTCTTTTATCTATATGGAATAAAGAGAGGC	3293
DB	3231	TGICTTACTAAGTCTGTTTGTGAATCTCCCTCATTTTATATGAATAAAGAGAGGC	3290
QY	3294	AGTCATGTTAGCAAAATGACAGTTAATATATCCCTAGCAGAGCGTGTGTTCACTTCCTGT	3353
DB	3291	AGTCATGTTATCAACGGCGTGCTATTTTCTTAGCTCACCCTTGGTCCACCTGCCTGT	3350
QY	3354	CGATCCCTCTGAGGATATGCCCATCGAAGCTTTTAGGCCATCTTTGATGGAAACAGAT	3413
DB	3351	AGAAACCTTCGGAGGATATGCCCTTCTAAGACTTTTCAGGCCACTCTTGATGGAATTCGAC	3410
QY	3414	CCC-----TGCCCTGACTGTCCAGCTATCCCTGAAAGTCGATCAGATTATAAATCG	3463
DB	3411	ACCCTCCCTCAACCCATGACTATCGAATGCTCGAATGGGATCAGGTTATAAATG	3470
QY	3464	GATTACATGTAATGTTTGGTTGTGT-TCTATCAACCCCAAGAGTTCCTTAAACTTG	3522
DB	3471	GATTGCATATGACTGTGTGCTGTGTGTGTCACTGGACAGAGTTCTCTAAACCTT	3530
QY	3523	CTTCAGTTATAGTAATCTGATGTTATATTCATTCAGAAG-----GCCATAAGTCAGT	3575
DB	3531	CTTTAGTTGTAGCAAGTTCTGTATCTCTCAATTCAGAAGCCCAAGGAGCATTTGGGTGACT	3590
QY	3576	TGAGTATTTTCATCCCTAGATAAGAAATCAAAATCAGCAGGAACT--GGTCATACAGGTA	3634
DB	3591	CGATCAAGGTTAAACCTTAGGAGAAATGCAATAAGTAGGAATCGGTGAGCAGAGGTA	3650
QY	3635	AGCACGAGGACAATAAGGATTTTTATAGATAF-----AATTTAATTTTTTTTATTGG	3687
DB	3651	AGCACGAGAGATGATAAGGATTTTATATAAATATATATAAATTAATTTTTTTGTTATGG	3710
QY	3688	TTAAGGAGACAATTTTGGAGAGCAAGCAATCTTTT	3723
DB	3711	TTA--TAGACAATTTTGGAAAGCAAGAGAACTCACT	3744

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Job time : 2636 secs





GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
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 Gapop 10.0 , Gapext 1.0  
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 Maximum Match 100%  
 Listing first 45 summaries

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 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2501.6	65.9	4457	12	US-11-136-527-2981
2	944.8	24.9	4275	12	US-11-136-527-2433
3	495.6	13.1	2802	12	US-11-136-527-2526
4	495.4	13.1	1797	9	US-11-198-640A-3
5	488.6	12.9	1797	9	US-11-198-640A-1
6	367	9.7	2464	9	US-11-245-147-139
7	367	9.7	2464	12	US-11-091-883-107
8	365.2	9.6	3518	12	US-11-136-527-2799
9	342.6	9.0	1821	9	US-11-245-147-64
10	109.6	2.9	2879	12	US-11-124-368A-166
11	109.4	2.9	2330	12	US-11-166-412-3
12	109.4	2.9	3113	12	US-11-091-883-30
13	109.4	2.9	3113	12	US-11-091-883-176
14	109.4	2.9	4916	12	US-11-166-412-4
15	109.4	2.9	5054	12	US-11-166-412-5
16	108	2.8	1251	12	US-11-136-527-996
17	106.6	2.8	1400	12	US-11-136-527-4231
18	106.6	2.8	1604	12	US-11-136-527-135
19	106.2	2.8	2138	12	US-11-136-527-2138
20	106	2.8	1563	12	US-11-136-527-1995

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2501.6	65.9	4457	12	US-11-136-527-2981	Sequence 2981, App
2	944.8	24.9	4275	12	US-11-136-527-2433	Sequence 2433, App
3	495.6	13.1	2802	12	US-11-136-527-2526	Sequence 2526, App
4	495.4	13.1	1797	9	US-11-198-640A-3	Sequence 3, Appli
5	488.6	12.9	1797	9	US-11-198-640A-1	Sequence 1, Appli
6	367	9.7	2464	9	US-11-245-147-139	Sequence 139, App
7	367	9.7	3518	12	US-11-091-883-107	Sequence 107, App
8	365.2	9.6	3254	12	US-11-136-527-2799	Sequence 2799, App
9	342.6	9.0	1821	9	US-11-245-147-64	Sequence 64, Appli
10	109.6	2.9	2879	12	US-11-124-368A-166	Sequence 166, App
11	109.4	2.9	2330	12	US-11-166-412-3	Sequence 3, Appli
12	109.4	2.9	3113	12	US-11-091-883-30	Sequence 30, App
13	109.4	2.9	3113	12	US-11-091-883-176	Sequence 176, App
14	109.4	2.9	4916	12	US-11-166-412-4	Sequence 4, Appli
15	109.4	2.9	5054	12	US-11-166-412-5	Sequence 5, Appli
16	108	2.8	1251	12	US-11-136-527-996	Sequence 996, App
17	106.6	2.8	1400	12	US-11-136-527-4231	Sequence 4231, App
18	106.6	2.8	1604	12	US-11-136-527-135	Sequence 135, App
19	106.2	2.8	2138	12	US-11-136-527-2138	Sequence 2138, App
20	106	2.8	1563	12	US-11-136-527-1995	Sequence 1995, App

No.	Score	Match Length	DB	ID	Description
1	2501.6	65.9	4457	12	US-11-136-527-2981
2	944.8	24.9	4275	12	US-11-136-527-2433
3	495.6	13.1	2802	12	US-11-136-527-2526
4	495.4	13.1	1797	9	US-11-198-640A-3
5	488.6	12.9	1797	9	US-11-198-640A-1
6	367	9.7	2464	9	US-11-245-147-139
7	367	9.7	2464	12	US-11-091-883-107
8	365.2	9.6	3518	12	US-11-136-527-2799
9	342.6	9.0	1821	9	US-11-245-147-64
10	109.6	2.9	2879	12	US-11-124-368A-166
11	109.4	2.9	2330	12	US-11-166-412-3
12	109.4	2.9	3113	12	US-11-091-883-30
13	109.4	2.9	3113	12	US-11-091-883-176
14	109.4	2.9	4916	12	US-11-166-412-4
15	109.4	2.9	5054	12	US-11-166-412-5
16	108	2.8	1251	12	US-11-136-527-996
17	106.6	2.8	1400	12	US-11-136-527-4231
18	106.6	2.8	1604	12	US-11-136-527-135
19	106.2	2.8	2138	12	US-11-136-527-2138
20	106	2.8	1563	12	US-11-136-527-1995

Query Match	65.9%;	Score	2501.6;	DB	12;	Length	4457;	
Best Local Similarity	82.9%;	12;	Mismatches	546;	Indels	90;	Gaps	22
Matches 3132;	Conservative	12;	Mismatches	546;	Indels	90;	Gaps	22
Qy	46	CGGAGTCTCTGGCTTCGCGCGCCCCACCCCTCCAGCTCTCTCCCTCCAGCGCTGCTCTCTCCGCTCCGCCAT	105					
Db	1	CGGAGTCTCTGGCTTCGCGCGCCCCACCCCTCCAGCGCTGCTCTCTCTCCGCTCCGCCAT	60					
Qy	106	ACACAGAGCGGCTCACACCCGCTCCCTCACTTCGCACACACAGACACAAAGCGGCACACAG	165					
Db	61	ACACAGACACGCTCACACCCGCTCTCTTCACTTCGACACACAGACACACGCGGCTCACAC	120					
Qy	166	GTCGCGACACACACT--TCGCTCTCCGGCGGCTCACACCCCTCTTGGCTGAGGCCCTT	223					
Db	121	GTCGCGACACACACTCCACTCTCTCCGGCGGCTCACACCCCTCTCTCTCGGCGCCCTC	180					
Qy	224	GCCGCT----GCAGCGGGCGCGAGCTGGAGCGCCCTCCCGGCTCACTTTGCAACG	278					
Db	181	GCCGCTGTGCGCGCGCGCGCGCGACCGGACGCCCTCTCCAGGGCTCACTTTGCAACG	240					
Qy	279	CTGACGGTGCCGGCAGTGCGCGTGGAGGTGGAAACAGCGCGCGCATCTCTCCCCCTGGTC	338					

ALIGNMENTS

RESULT 1  
 US-11-136-527-2981  
 ; Sequence 2981, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 362830  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 2981  
 ; LENGTH: 4457  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-11-136-527-2981

Query Match	65.9%;	Score	2501.6;	DB	12;	Length	4457;	
Best Local Similarity	82.9%;	12;	Mismatches	546;	Indels	90;	Gaps	22
Matches 3132;	Conservative	12;	Mismatches	546;	Indels	90;	Gaps	22
Qy	46	CGGAGTCTCTGGCTTCGCGCGCCCCACCCCTCCAGCTCTCTCCCTCCAGCGCTGCTCTCTCCGCTCCGCCAT	105					
Db	1	CGGAGTCTCTGGCTTCGCGCGCCCCACCCCTCCAGCGCTGCTCTCTCTCCGCTCCGCCAT	60					
Qy	106	ACACAGAGCGGCTCACACCCGCTCCCTCACTTCGCACACACAGACACAAAGCGGCACACAG	165					
Db	61	ACACAGACACGCTCACACCCGCTCTCTTCACTTCGACACACAGACACACGCGGCTCACAC	120					
Qy	166	GTCGCGACACACACT--TCGCTCTCCGGCGGCTCACACCCCTCTTGGCTGAGGCCCTT	223					
Db	121	GTCGCGACACACACTCCACTCTCTCCGGCGGCTCACACCCCTCTCTCTCGGCGCCCTC	180					
Qy	224	GCCGCT----GCAGCGGGCGCGAGCTGGAGCGCCCTCCCGGCTCACTTTGCAACG	278					
Db	181	GCCGCTGTGCGCGCGCGCGCGCGACCGGACGCCCTCTCCAGGGCTCACTTTGCAACG	240					
Qy	279	CTGACGGTGCCGGCAGTGCGCGTGGAGGTGGAAACAGCGCGCGCATCTCTCCCCCTGGTC	338					

Db 241 CTGACAGAGCGGCGAGTGGCGGTGGAGGTGGGAAAGCTGGCGACATCTAGCCCCCTGGTC 300  
Qy 339 ACAGCCCAAGCCAGGACGCGCCGCGAACTCTTCGGCTGCTCTCCATGAGTCGGGATC 398  
Db 301 GCAGCGGAGACTGGACG-CTGCGGAACTCTCGCGCGCGCTCTCCATGAGTTGGGATC 359  
Qy 399 GCAGCATCCCCCACCAGCC--GCTCACCGCTTCGGGAGCGCTGGGCTTGTAACCGC 455  
Db 360 GCAGCATCCCCCAGCGCGCTGCTCACCGCTCTGGGAGCGCTGGGTTGTGACCGC 419  
Qy 456 AGCCCTTCGGGACAGCAGCTGTGACTCTCCCGCCAGTGCAGATTTTCGGGACAGCTCTCTA 515  
Db 420 AGCCCTTCGGGACAGCAGCTGTGACTCTCCCGCAATCCAGATTTTCGGGCTGCTCTA 479  
Qy 516 GAAACTCGCTTAAGACGGAACCGGCACAGCACTCAAGCCCACTGCGGAAGAGGGCAG 575  
Db 480 GAAACTCGCTTAAGACGGAACCTCCACAGAACCCAAAGCCCACTGCGGGAGAGCGCAG 539  
Qy 576 CCGCGCAGCCCGGCGCTGAGCTGGAACCTTAGGGTGCCGGCAGCA-----CTGC 629  
Db 540 CCGGACAGCCCGGCGCTGAGCTGGACCTTCAACAGAGCGGGCCAGCACAGCGCGGC 599  
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Qy 690 CCGCAGCCCAACATTCAGCGCGGAAGATPACCTTCAGATATGCCCTGGGTCAAAGCCCA 749  
Db 660 CCGCAGCCCAACATTCAGCGCGGAAGATPACCTTCAGATATGCCCTGGGTCAAAGCCCA 719  
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Qy 810 CACGAGATCATGAACCCCGACTACACCAAGCTGACCATGGACCTTGGCAGCACTGAGAT 869  
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Qy 870 CACGGCTACAGCCACCACTCTCGTCCCGCAGCATCAGTACTCTTCGTGGAGGGCTACTCGAG 929  
Db 840 CATGGCCACGGCCACGACCTCTCGTCCCGCAGCTTCAGTACTCTTCATGGAGGGCTACCCCGAG 899  
Qy 930 CAACTACGAATCATAGCCTTCTCGGTGTACCAATGACG-----CGGCCCTT 977  
Db 900 CAGCTGCGAACTCAAGCCCTCTCTGCTGTACCAATGCGCCCTTCTGGGCCCTTCGGCCCTT 959  
Qy 978 GATCAAGTGGAGGGGGCGGCGGCCAGCTACCATCAACCATCAACCAACCAACCATCA 1037  
Db 960 GATCAAGATGGAAGAGGGTCCGAGCATGGCTACCAACCAACCAACCAACCATCA 1019  
Qy 1038 CCACGACCAACATACACGAGAGCATCAGCAGCCATCCATCTCCAGCCTCCAGGCC 1097  
Db 1020 TCATCACCAACCAACCAAGCAG-----CAGCAGCGCTCATTTCTCTCTCTGGGCC 1073  
Qy 1098 GGAGGACGAGGTGCTGCCAGCAGCTCCATGATTTCAAGCAGTCCCAACCGTCCACGCC 1157  
Db 1074 CGAGGACGAGGTACTGCCAGCAGCTCCATGATTTCAAGCAGTCTCCGCCGTCTACGCC 1133  
Qy 1158 CACACGCGCGCTTCCCCCGCAGCGGGGGGCTTATGGGACGAGGCACTGCCCTCGGC 1217  
Db 1134 GACCACTCCAGGCTTCCCCCGCAGCGGGGGGCTGTGGGACGAGCTGCCCTCTGC 1193  
Qy 1218 GCCCGCTGATGCAACCGCGCGCTGTGACCCCGCGATGAAGCGGCTCCCAAGGT 1277  
Db 1194 GCCTGCTGATCGCTCCCGGACCGCTGTGGACCCCGCAGATGAAGGCACTGCCCCAT 1253  
Qy 1278 GCGCGCGCGCTTCCCGCTCTTCCATTTCAAGCCCTCCCGCGCATCCCGCGGCC 1337  
Db 1254 GCGCGCTGCTGGCGCTTCCCGATCTTCTTCAAGCCCTCACCGCACACCTCCCGCGCC 1313  
Qy 1338 CAGCCCGCGCGGCCACCACTCGGCTACGACCCGAGCGCGCTGCGCGCTCAGCT 1397  
Db 1314 CAGCCCGCGCGGCCACCACTCGGCTATGACCCCAACCGCGCGAGCTGCGCTCAGTCT 1373

Qy 1398 GCCGTGGGAGCCGAGCCGCGCGGCGAGCGCGCGCTTGAGAGCACCCGTA 1457  
Db 1374 ACCCTGGGAGCCGCGCGCGGCGAGCAAGACTGCTGCTCGAGGGCCATCCGTA 1433  
Qy 1458 CGGCTGCGCTGCGCAAGAGGCGGCGCTTCGCGCTTCGCGCTTCGCGCTCACGCC 1517  
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Qy 1518 CTCCTTACCGCGTCCAGCTGCTGGGCGAGAGTCCAGCCTGCGCTGCGCGCCAGCAG 1577  
Db 1494 GTCCCTTACCGCGTCCAGCTGCTGGGAGAGAGCCCAAGCTTACCATCGCCCAATAG 1553  
Qy 1578 GAGCTGCTGCTGGCGAGGSCACGTGTGCCGTGTGGGGGACAAACGCGCGCTGCCAGCA 1637  
Db 1554 GAGCTCATCATCCGCGAGGGGACGTGTGTGTGTGGGGGACAAATGTGCTGCTGCAGCA 1613  
Qy 1638 CTACGGCGTGCAACTTCGCGAGGGCTGCAAGGGCTTTTCAAGAGAACAGTGCAGAAAA 1697  
Db 1614 CTACGGAGTCCGCACTTCGCGAGGGCTGCAAGGGCTTCTTCAAGAGAACGGTGCAGAAAA 1673  
Qy 1698 TGCAAATATGTTTTCCTGGCAAAATAAAACTGCCCAAGTAGACAGAGACGTCGAAAA 1757  
Db 1674 CGCAAAATATGTTTTCCTGGCAAAATAAAACTGCCCGGTAGACAGAGACGTCGAAATCG 1733  
Qy 1758 ATGTCAGTACTGTCGATTTTCAAGAGTGTCTCAGTGTGGAAATGTTAAAGAGTTGTCG 1817  
Db 1734 ATGTCAGTACTGTCGAGTTTTCAGAAAGTGTCTCAGTGTGGGATGTTGAAGAGTTGTCG 1793  
Qy 1818 TACAGATAGTCTGAAGGGGAGAGGTCGTCTGCTTCCAAACCAAGAGAGCCCAATACA 1877  
Db 1794 TACAGATAGTCTGAAGGGGAGAGGTCGTCTGCTTCCAAACCAAGAGAGCCCACTACA 1853  
Qy 1878 ACAGAACTTCTCAGCCCTCTCCAACCTTCTCTCCAATCTGCAATGATGAATGTCCTTGT 1937  
Db 1854 ACAGGAGCCCTCGCAGCCCTCTCCACCATCTCTCCGATCTGTATGATGAACCGCCTTGT 1913  
Qy 1938 CCGAGCTTTTACAGACTCAACACCCAGAGATCTTGATTTATTCAGATACTGTCACACTGA 1997  
Db 1914 CCGAGCTTTTACAGACGCAACCGCCAGAGACTTGATTTACTCCAGATACTGTCACCGGA 1973  
Qy 1998 CCAGGCTCTGCGAGCAGAGATGCTGAGCATGTGCAACAAATTTCTACAACTCTCTGACAGC 2057  
Db 1974 CCAGGCTCTGCGGCGCAGAGCTGAGCACTGCGAGCAGTCTTACAACTCTCTGACGCGC 2033  
Qy 2058 CTCCTTGAATGATCCAGAACTGGGCGCAAAAGATTCGGGATTTTATGATCTCTCCCAA 2117  
Db 2034 CTCCTTGAATGATCCAGAACTGGGCGCAAAAGATTCGGGATTTTCACTGATCTCTCCCAA 2093  
Qy 2118 AGAGATCAGACATTTACTTATGATCAGCCCTTTTGGAGCTGTTTGTCTCAGACTTTC 2177  
Db 2094 AGAGATCAGACATTTACTTATGATCAGCCCTTTTGGAGCTGTTTGTCTTACTACTT 2153  
Qy 2178 CATCAGGTCAAACTGCTGAAGATAAGTTTGTGTTCTGCAATGAGCTTGTCTGATCG 2237  
Db 2154 TATCAGGTCAAACTGCTGAAGATAAGTTTGTGTTCTGCAATGAGCTTGTCTGACCG 2213  
Qy 2238 ACTTCAGTGCCTTCTGTAATTTGGGAGTGGCTGCACTCTATTAAGACTTTTCTTAAA 2297  
Db 2214 ACTTCAGTGCCTTCTGCGGATTTGGGAGTGGCTGCACTCTTAAAGACTTTTCTTAAA 2273  
Qy 2298 TTTTGAGAGCTGAACTTGTATATCCAGCCCTTAGCCCTGCTGTCAGACTGAGCATGAT 2357  
Db 2274 TTTTGAGAGCTGAACTTGTATATCCAGCCCTTAGCCCTGCTGTCAGACTGAGTATGAT 2333  
Qy 2358 CACAGAAAGACATGGTTTAAAGAAACCAAGAGAGTTCGAAGAGCTATGCAACAAGATCAC 2417  
Db 2334 CACAGAGGACATGGTTTAAAGAAACCAAGAGAGTGGGAGGCTATGCAACAAGATCAC 2393  
Qy 2418 AAGCAGTTTAAAGACCAACAGAGTAAGGAGCAGGCTCTGGAGGCCACCGAGTCCAGGT 2477  
Db 2394 AAGCAGTTTAAAGGACCAACAGAGTAAGGAGCAGGCTTGTGGAGGCCCTCAGAGCCCMWSET 2453